

FIGURE 1

A. CTTATCGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT
CACAAATTTACAAATAAAGCATTGTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA
++++++
ATGTATCTTATCATGTC (Seq ID NO:1) ↑ Cleavage site

B. AAUAAA
++++++
GCA

C. (Seq ID NO:18)
GCAaaaaaaaaaaaaaaaaaaaaa

+ Upstream and downstream
cleavage-polyadenylation elements



FIGURE 2

► ITR

```

CATCATCAAT  AATATACCTT  ATTTTGGATT  GAAGCCAATA  TGATAATGAG  GGGGTGGAGT  60
TTGTGACGTG  GCGCGGGGCG  TGGGAACGGG  GCGGGTGACG  TAGTAGTGTG  GCGGAAGTGT  120
GATGTTGCAA  GTGTGGCGGA  ACACATGTAA  GCGACGGATG  TGGCAAAAGT  GAC G TTTTGT  180
GTGTGCGCCG  GTGTACACAG  GAAGTGACAA  TTTTCGCGCG  GTTTTAGGCG  GATGTTGTAG  240
TAAATTTGGG  CGTAACCGAG  TAAGATTGG  CCATTTTCGC  GGGAAACTG  AATAAGAGGA  300
AGTGAAATCT  GAATAATTTT  GTGTTACTCA  TAGCGCGTAA  TATTGTCTA  GGGCCGCGGG  360
GACTTTGACC  GTTTACGTGG  AGACTCGCCC  AGGTGTTTTT  CTCAGGTGTT  TTC CGC GTTC  420
CGGGTCAAAG  TTGGCGTTTT  ATTATTATAG  TCAGCTGACG  TGTAGTGTAT  TTA TAC CCGG  480
TGAGTTCCTC  AAGAGGCCAC  TCTTGAGTGC  CAGCGAGTAG  AGTTTCTCC  TCC GAG CCGC  540
TCCGACACCG  GGACTGAAA A  TGAGACATAT  TATCTGCCAC  GGAGGTGTTA  TTACCGAAGA  600

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• Enhancer elements

X E2F-motif

+ Packaging elements

dl 103-551 **Ar6**

dl 189-551

dl 357-551 **Ar5**

(SEQ ID NO:2)



FIGURE 3A

1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----

61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
+-----ITR-----+

121 CGATACCGTCGAAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----

181 ACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----

241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATCATCCGGACAAAGCCTGC
-----+-----

301 GCGCGCCCCGCCCCGCCATTGGCCGTACCGCCCCGCGCCGCGCCCCATCTCGCCCCCTCG
-----E2F-1 promoter-----

361 CCGCCGGGTCCGGCGCGTTAAAGCCAATAGGAACCGCCGCGTTGTTCCCGTCACGGCCG
-----E2F-1 promoter-----

421 GGGCAGCCAATTGTGGCGGCGCTCGGCGGCTCGTGGCTCTTTTCGCGGCAAAAAGGATTTG
-----E2f-1 promoter-----

481 GCGCGTAAAAGTGGCCGGGACTTTGCAGGCAGCGGCGGGGGCGGAGCGGGATCGAG
-----E2f-1 promoter-----

541 CCCTCGATGATATCAGATCATCGGATCCCGGTCGACTGAAAATGAGACATATTATCTGCC
-----+-----

601 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
-----Ela gene-----

661 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCTTTCACGAAGTGT
-----Ela gene-----

721 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
-----Ela gene-----

781 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
-----Ela gene-----

841 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCT
-----Ela gene-----

901 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGG
-----Ela gene-----



FIGURE 3B

961 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
-----Ela gene-----

1021 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTTCATTATCACCGGAGGAATACGGGGGACC
-----Ela gene-----

1081 CAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
-----Ela gene-----

1141 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTTTTTTAAT
-----Ela gene-----

1201 TTTTACAGTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTTAAAAGGTCCTGTGTC
-----Ela gene-----

1261 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA
-----Ela gene-----

1321 AATGGCGCCTGCTATCCTGAGACGCCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
-----Ela gene-----

1381 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC
-----Ela gene-----

1441 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG
-----Ela gene-----

1501 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG
-----Ela gene-----

1561 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTGTGAATGAGT
-----Ela gene-----

1621 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC
-----+-----

1681 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA
-----Ela gene-----

1741 GGCTTGGGAGTGTTTGAAGATTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA
-----Ela gene-----

1801 CA
--



FIGURE 3C

33881 AACCTACGCCCAGAAACGAAAGCCAAAAAACCCACAACCTTCCTCAAATCGTCACTTCCGT

33941 TTTCCACGTTACGTCACTTCCCATTTTTAATTAAGAATTCTACAATTCCCAACACATACA

34001 AGTTACTCCGCCCTAAAACCCTGGGCGAGTCTCCACGTAAACGGTCAAAGTCCCCGCGGC
+--packaging signal-----

34061 CCTAGACAAATATTACGCGCTATGAGTAACACAAAATTATTCAGATTTCACTTCCTCTTA
-----packaging signal-----

34121 TTCAGTTTTCCCGCGAAAATGGCCAAATCTTACTCGGTTACGCCCAAATTTACTACAACA
-----packaging signal-----

34181 TCCGCCTAAAACCGCGCGAAAATTGTCACCTCCTGTGTACACCGGCGCACACCAAAAACG
-----+

34241 TCACTTTTGCCACATCCGTCGCTTACATGTGTTCCGCCACACTTGCAACATCACACTTCC

34301 GCCACACTACTACGTCACCCGCCCCGTTCACGCCCCGCGCCACGTCACAAACTCCACC
+-----ITR-----

34361 CCCTCATTATCATATTGGCTTCAATCCAAAATAAGGTATATTATTGATGATG
-----ITR-----+



FIGURE 4

1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----

61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGCCGCTAGCGAT
-----ITR-----++-----MCS-----

121 ATCGGATCCCGGTGCGACTGAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGA
-----+-----E1a-----

181 AGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCC
-----E1a-----

241 ACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGC
-----E1a-----

301 CCCCAGAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGC
-----E1a-----

361 GGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCC
-----E1a-----

421 TCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCC
-----E1a-----

481 AAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGA
-----E1a-----

541 CGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGG
-----E1a-----

601 TTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCT
-----E1a-----



FIGURE 5

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1  CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
   +-----ITR-----

61  TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
   -----ITR-----+-----+-----

121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
   -----polyA-----

181 ACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
   -----polyA-----

241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATATCGGATCCCGGTCTGACT
   -----+-----+-----

301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCT
   -----Ela-----

361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGA
   -----Ela-----

421 ACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGA
   -----Ela-----

481 GGAGGCGGTTTTCGCAGATTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGA
   -----Ela-----

541 CTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCC
   -----Ela-----

601 CGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGT
   -----Ela-----

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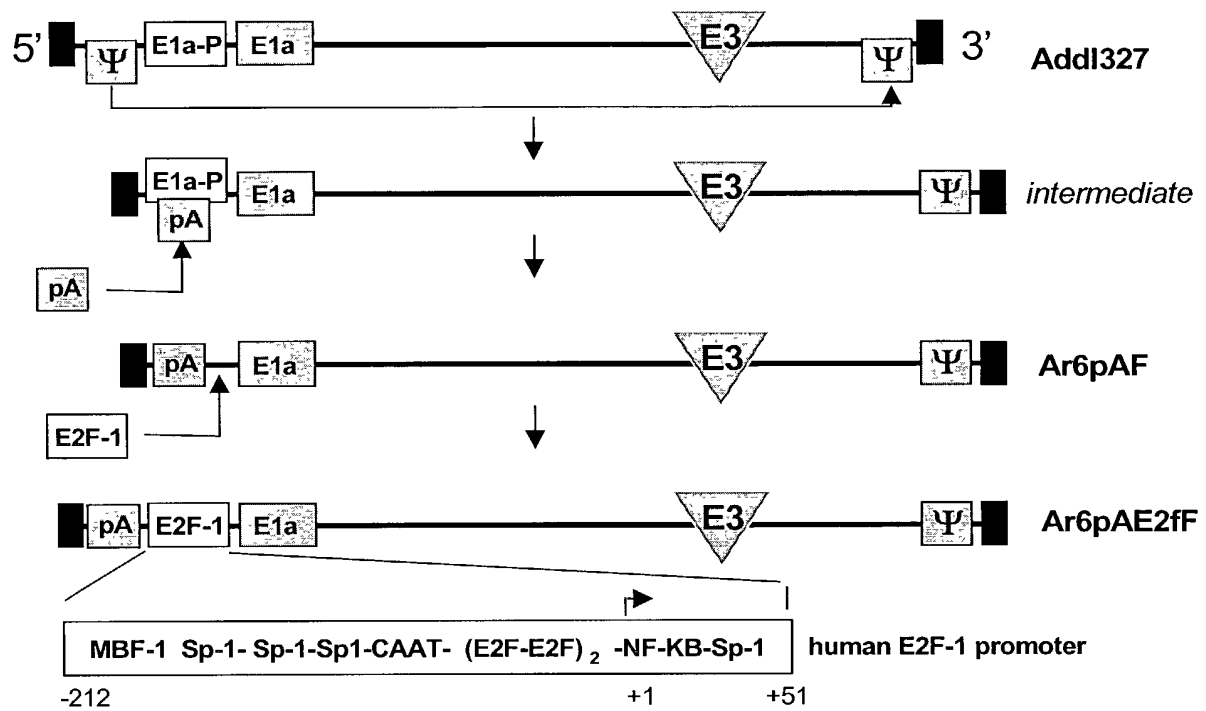
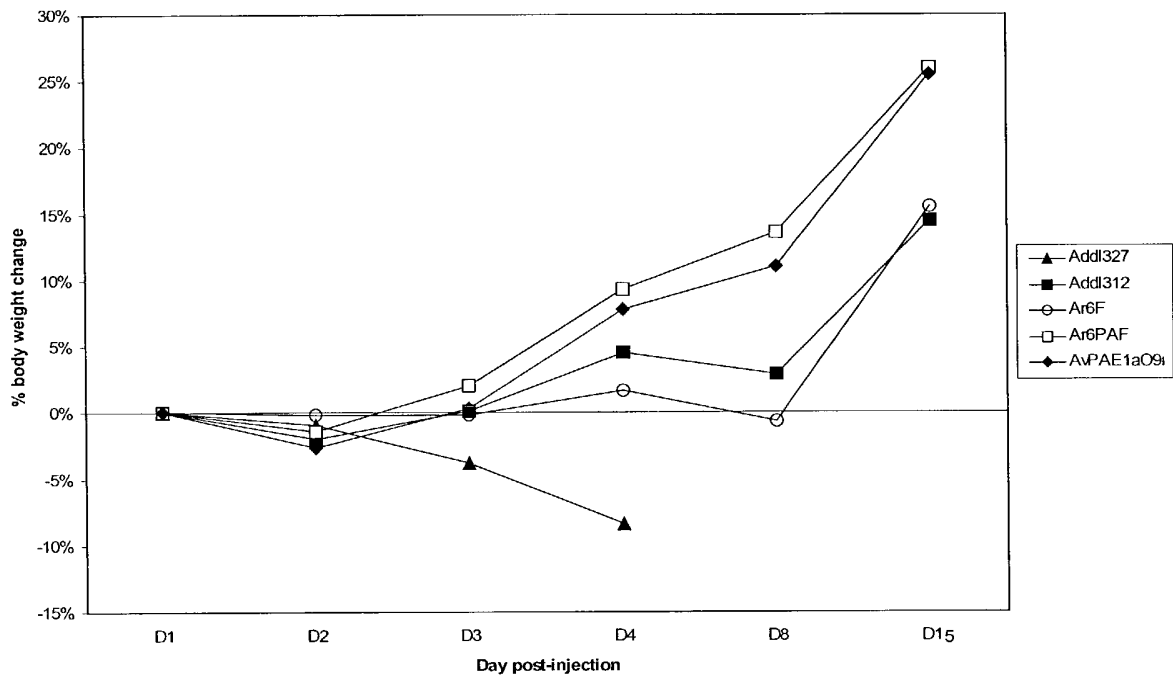


FIGURE 6



Fig. 7 Body weight change



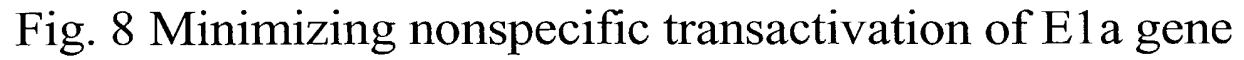


Figure 9. Mean H460 tumor volume

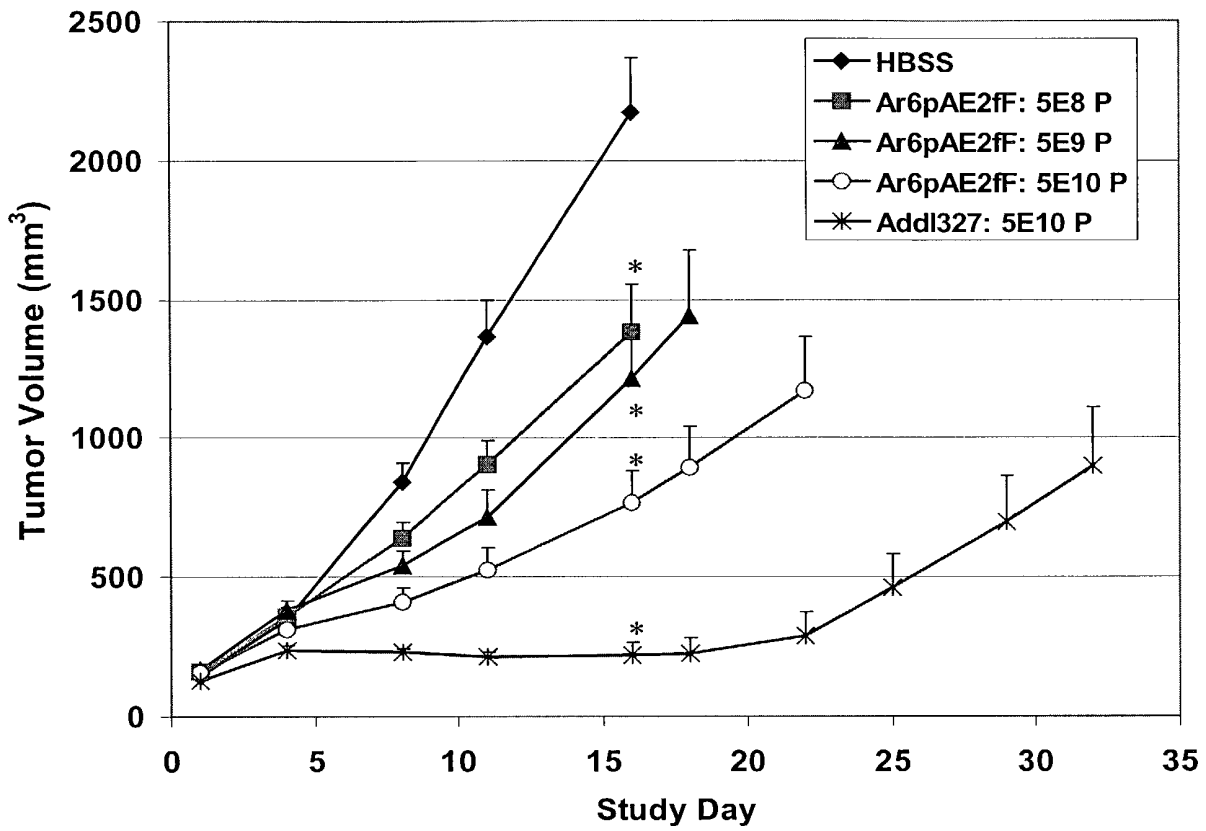
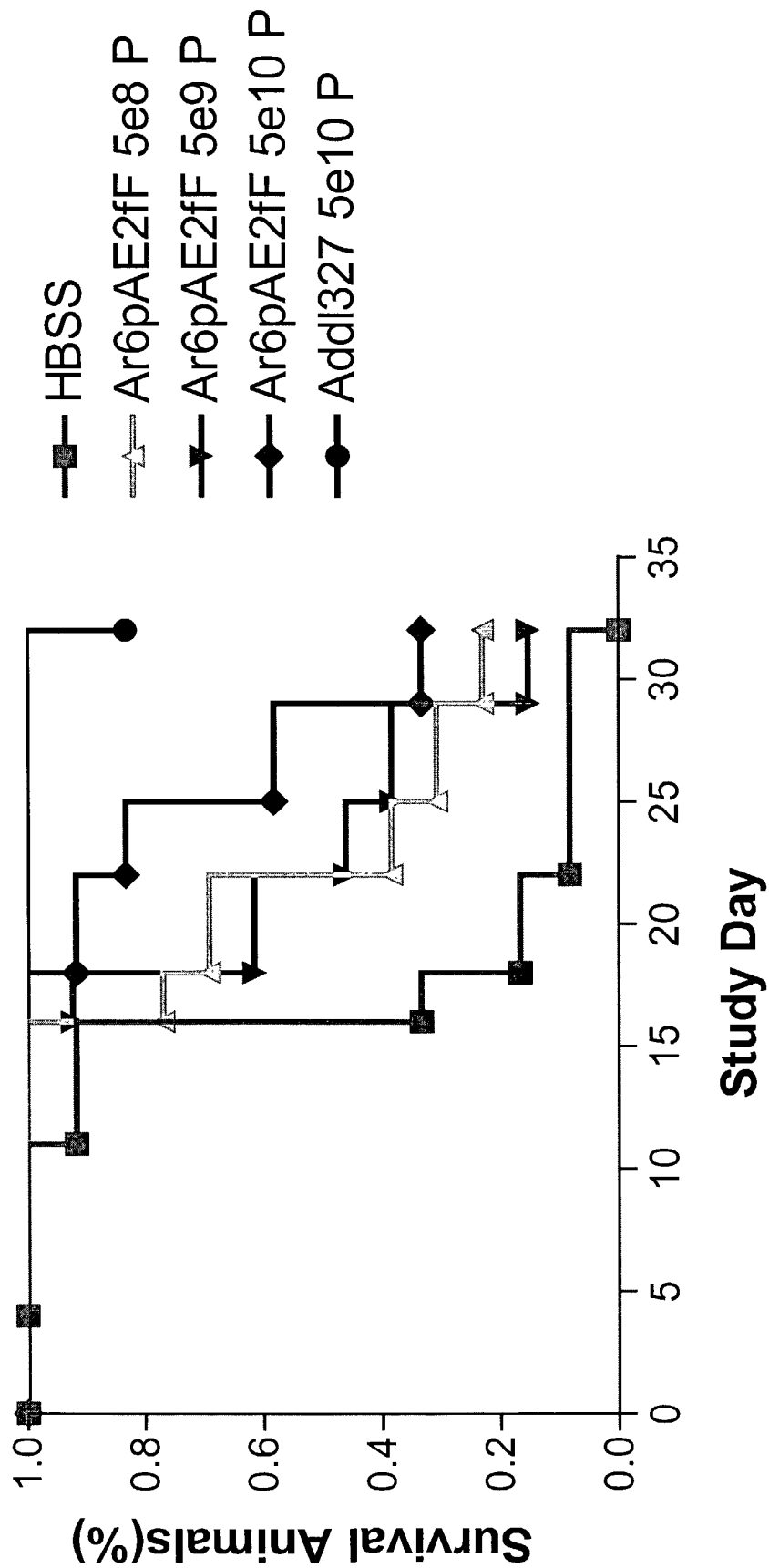


FIGURE 10



$$= \frac{1}{n} \sum_{j=1}^n \left(\frac{\partial}{\partial x_j} \right)^2 f(x) = \frac{1}{n} \sum_{j=1}^n \left(\frac{\partial}{\partial x_j} \right)^2 f(x) = \frac{1}{n} \sum_{j=1}^n \left(\frac{\partial}{\partial x_j} \right)^2 f(x)$$


Figure 1 is a line graph showing Percent Survival (Y-axis, 0 to 100) versus Time (Days) (X-axis, 0 to 40). The graph compares the survival of mice in five different groups over a 40-day period. The groups are: HBSS (dashed line with open circles), Ar6pAE2fF 5E8 (solid line with open circles), Ar6pAE2fF 5E9 (solid line with open triangles), Ar6pAE2fF 5E10 (solid line with open diamonds), and Addl327 5E10 (solid line with open circles). The HBSS group shows a rapid decline in survival, reaching 0% by day 30. The other groups show significantly higher survival rates, remaining above 50% throughout the 40-day period.

Time (Days)	HBSS	Ar6pAE2fF 5E8	Ar6pAE2fF 5E9	Ar6pAE2fF 5E10	Addl327 5E10
0	100	100	100	100	100
5	100	100	100	100	100
10	100	100	100	100	100
15	100	100	100	100	100
20	100	100	100	100	100
25	100	100	100	100	100
30	0	100	100	100	100
35	0	100	100	100	100
40	0	100	100	100	100



FIGURE 13

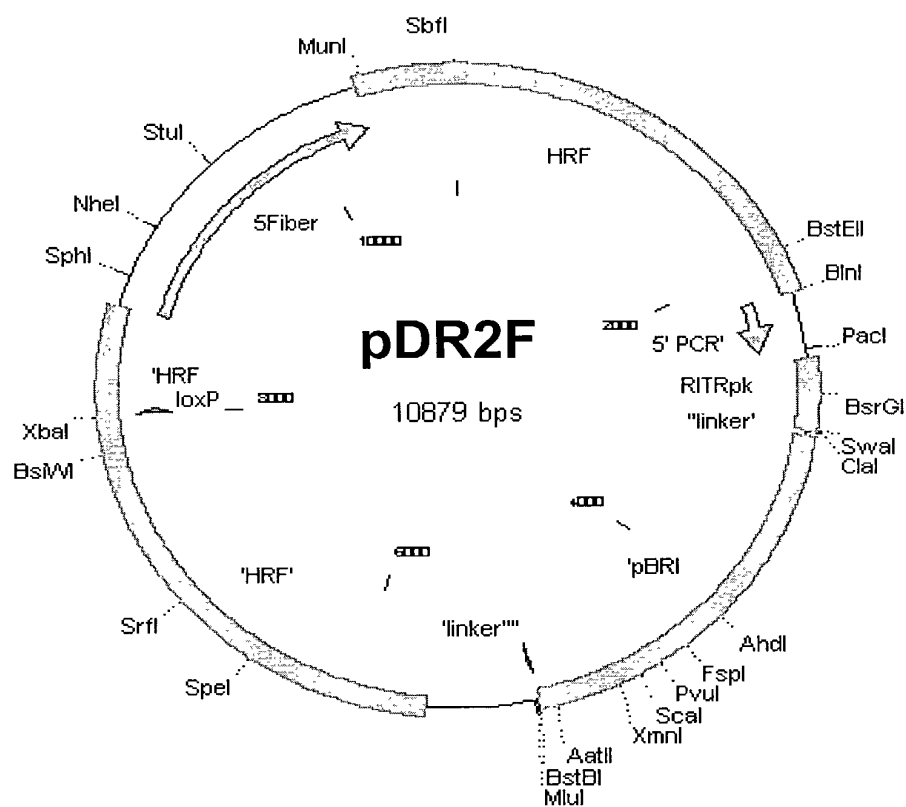




FIGURE 15

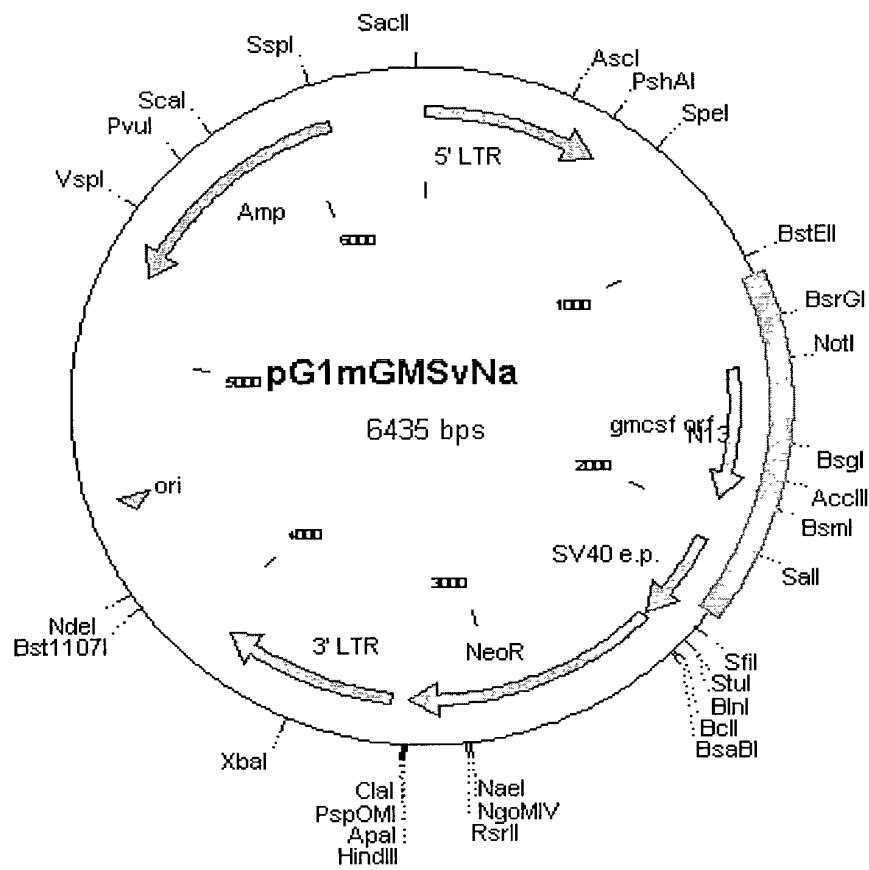


FIGURE 16

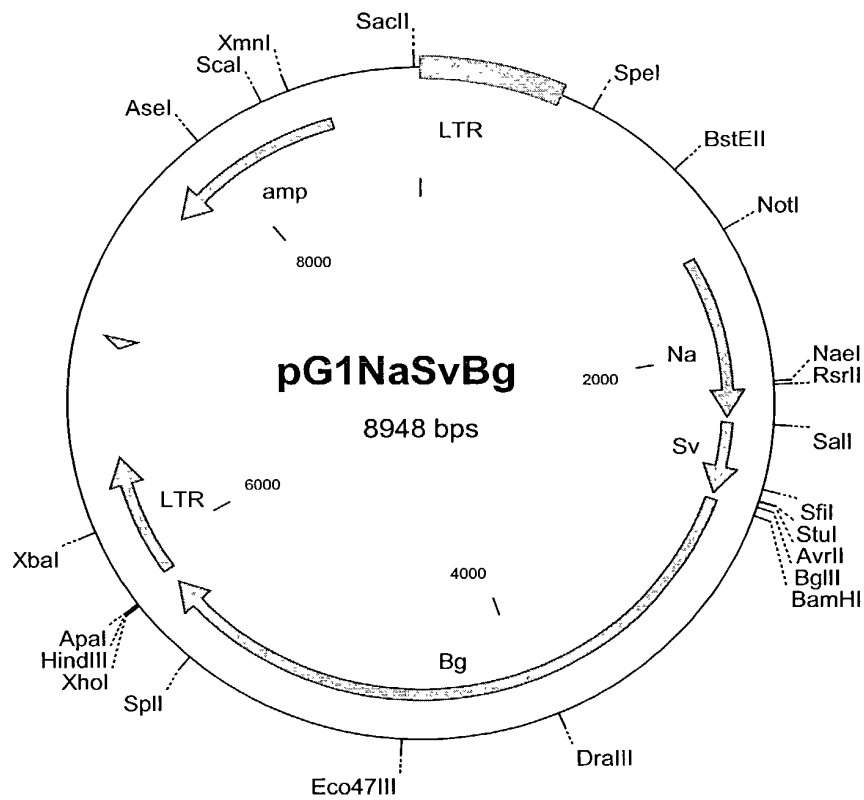


FIGURE 17

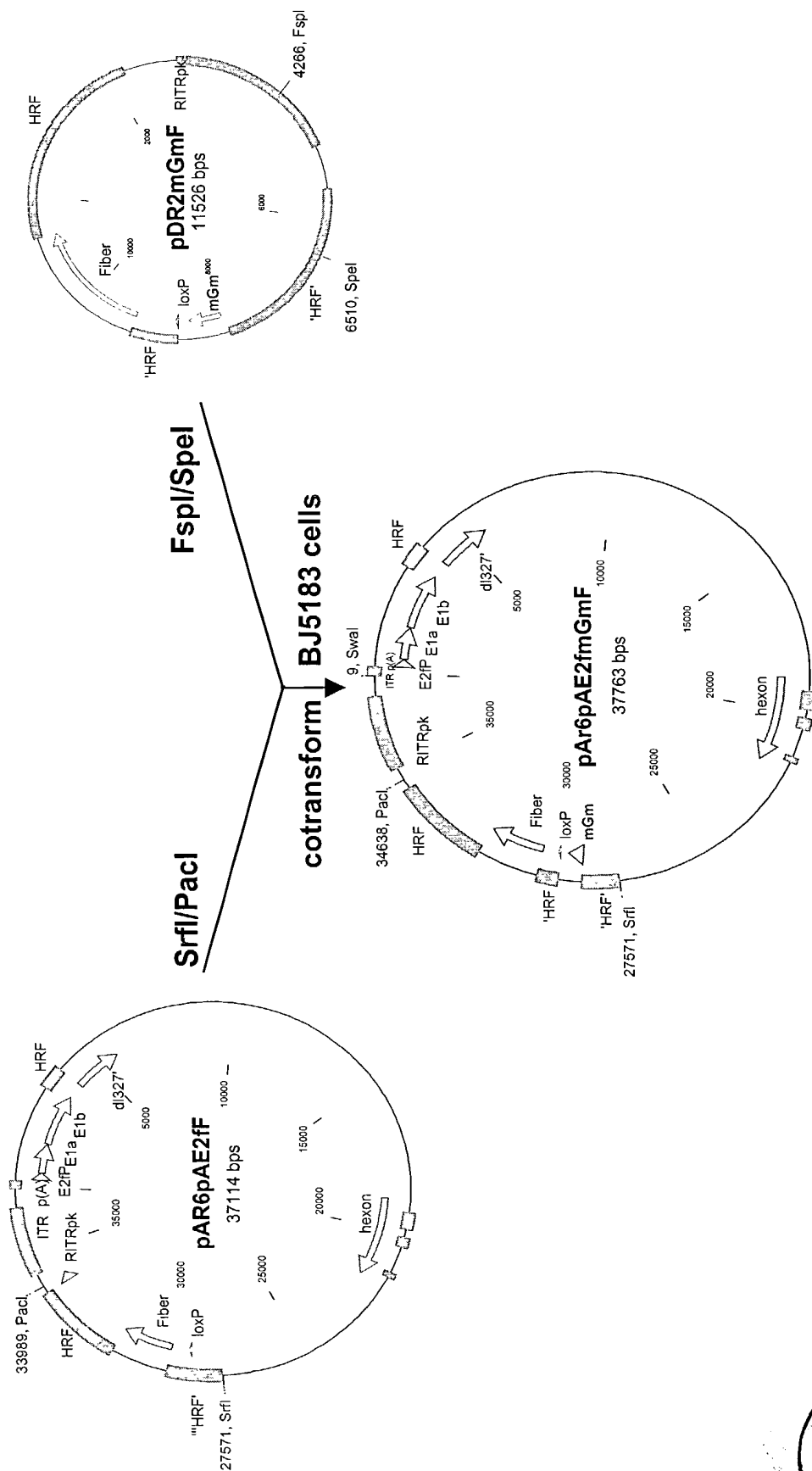
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7928 GAAAACCCTT AGGGTATTAG GCCAAAGGCG CAGCTACTGT GGGGTTTATG
7978 AACAAATTCAG GCAACTCTAC GGGCTATTCT AATTCAGGTT TCTCTAGCCG
8028 GGCTGCAGGA ATTCGATGGC CGCTACCTAC AATGGCCCAC GAGAGAAAGG
      M A H E R K
8078 CTAAGGTCCT GAGGAGGATG TGGCTGCAGA ATTTACTTTT CCTGGGCATT
      A K V L R R M W L Q N L L F L G I
8128 GTGGTCTACA GCCTCTCAGC ACCCACCCGC TCACCCATCA CTGTCACCCG
      V V Y S L S A P T R S P I T V T
8178 GCCTTGAAG CATGTAGAGG CCATCAAAGA AGCCCTGAAC CTCCTGGATG
      R P W K H V E A I K E A L N L L D
8228 ACATGCCTGT CACATTGAAT GAAGAGGTAG AAGTCGTCTC TAACGAGTTC
      D M P V T L N E E V E V V S N E F
8278 TCCTTCAAGA AGCTAACATG TGTGCAGACC CGCCTGAAGA TATTCGAGCA
      S F K K L T C V Q T R L K I F E
8328 GGGTCTACGG GGCAATTTCA CCAAACCTCAA GGGCGCCTTG AACATGACAG
      Q G L R G N F T K L K G A L N M T
8378 CCAGCTACTA CCAGACATAC TGCCCCCCTAA CTCCGGAAC GGAAGTGTAA
      A S Y Y Q T Y C P P T P E T D C E
8428 ACACAAGTTA CCACCTATGC GGATTTCATA GACAGCCTTA AAACCTTTCT
      T Q V T T Y A D F I D S L K T F
8478 GACTGATATC CCCTTTGAAT GCAAAAAACC AGTCCAAAAA TGAGGAAGCC
      L T D I P F E C K K P V Q K -
8528 CAGGCCAGCT CTGAATCCAG CTTCTCAGAC TGCTGCTTTT GTGCCTGCGT
8578 AATGAGCCAG GAACTCGGAA TTTCTGCCTT AAAGGGACCA AGAGATGTGG
8628 CACAGGTAGT CGAATCAAGC TTATCGATAC CGTCGACCTC GACTAGATAA
8678 CTTTCGTATAA TGTATGCTAT ACGAAGTTAT GCTAGAAATG GACGGAATTA
8728 TTACAGAGCA GCGCCTGCTA GAAAGACGCA GGGCAGCGGC CGAGCAACAG
8778 CGCATGAATC AAGAGCTCCA AGACATGGTT AACTTGCACC AGTGCAAAA 8826

```



FIGURE 18



[illegible]

FIGURE 20

28536 TATTAGGCCA AAGGCGCAGC TACTGTGGGG TTTATGAACA ATTCAAGCAA
 28586 CTCTACGGGC TATTCTAATT CAGGTTTCTC TAGGATCTTT CCGCAGCAGC

28636 CGCCACCATG TGGCTGCAGA GCCTGCTGCT CTTGGGCACT GTGGCCTGCA
 M W L Q S L L L L G T V A C

28686 GCATCTCTGC ACCCGCCCCG CCGCCAGCC CCAGCACGCA GCCCTGGGAG
 S I S A P A R S P S P S T Q P W E

28736 CATGTGAATG CCATCCAGGA GGCCCGGCGT CTCCTGAACC TGAGTAGAGA
 H V N A I Q E A R R L L N L S R

28786 CACTGCTGCT GAGATGAATG AAACAGTAGA AGTCATCTCA GAAATGTTTG
 D T A A E M N E T V E V I S E M F

28836 ACCTCCAGGA GCCGACCTGC CTACAGACCC GCCTGGAGCT GTACAAGCAG
 D L Q E P T C L Q T R L E L Y K Q

28886 GGCCTGCGGG GCAGCCTCAC CAAGCTCAAG GGCCCCTTGA CCATGATGGC
 G L R G S L T K L K G P L T M M

28936 CAGCCACTAC AAGCAGCACT GCCCTCCAAC CCCGGAAACT TCCTGTGCAA
 A S H Y K Q H C P P T P E T S C A

28986 CCCAGACTAT CACCTTTGAA AGTTTCAAAG AGAACCTGAA GGA CTTTCTG
 T Q T I T F E S F K E N L K D F L

29036 CTTGTCATCC CCTTTGACTG CTGGGAGCCA GTCCAGGAGT GAGTCGACAA
 L V I P F D C W E P V Q E -

29086 GCTCTAGATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGCTAGAAAT
 29136 GGACGGAATT ATTACAGAGC AGCGCCTGCT AGAAAGACGC AGGGCAGCGG
 29186 CCGAGCAACA GCGCATGAAT CAAGAGCTCC AAGACATGGT TAACTTGCAC
 29236 CAGTGCAAAA GGGGTATCTT TTGTCTGGTA AAGCAGG 29273



[illegible]

FIGURE 22

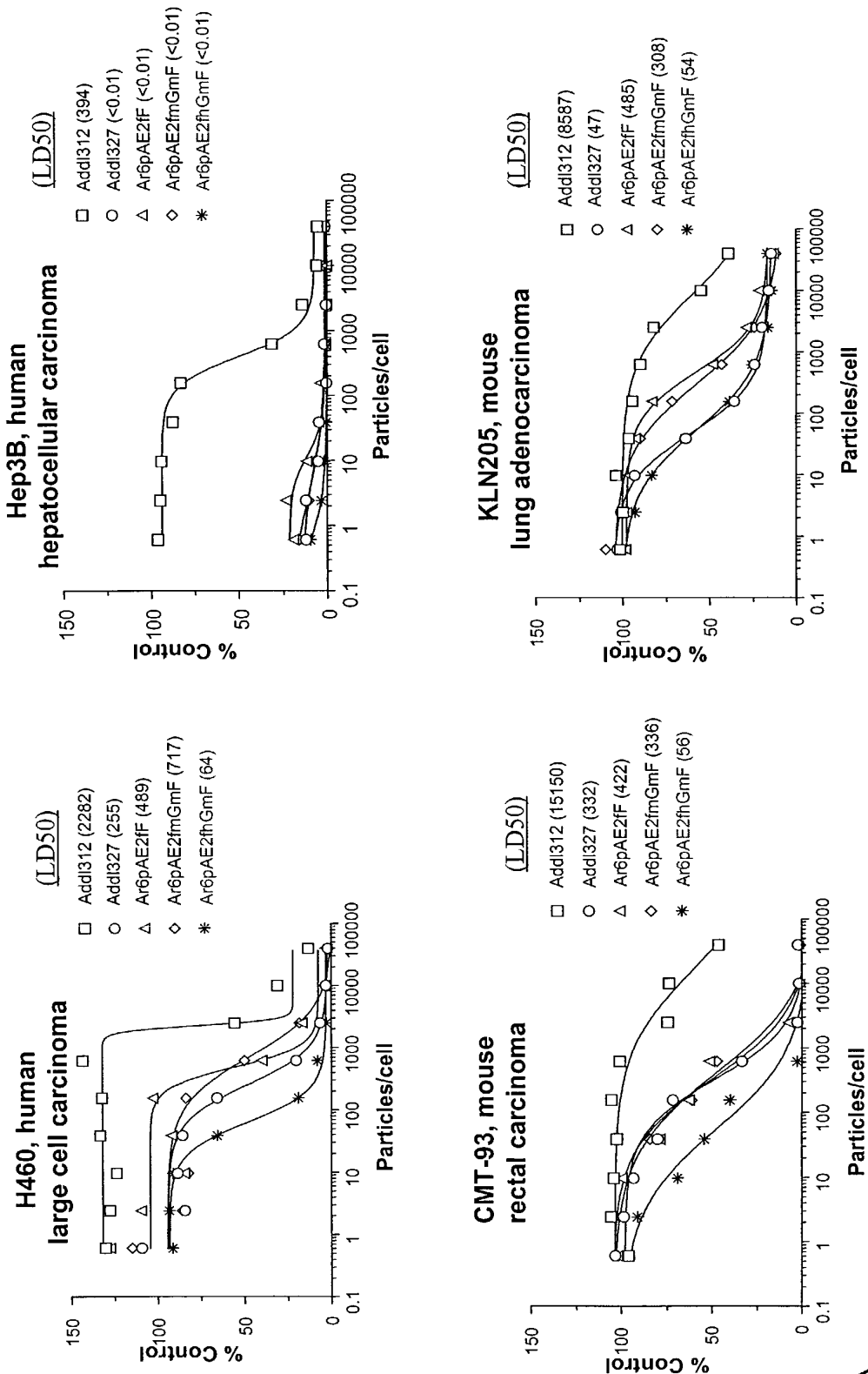


FIGURE 23

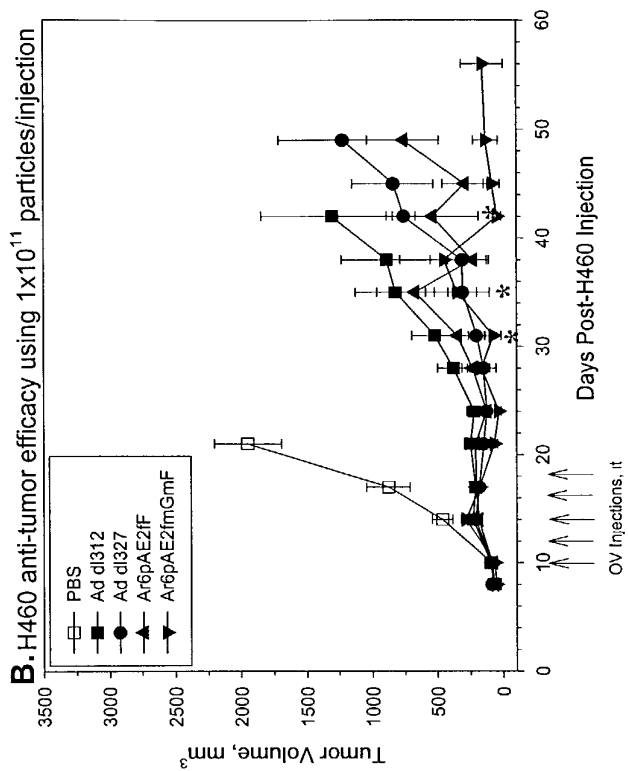
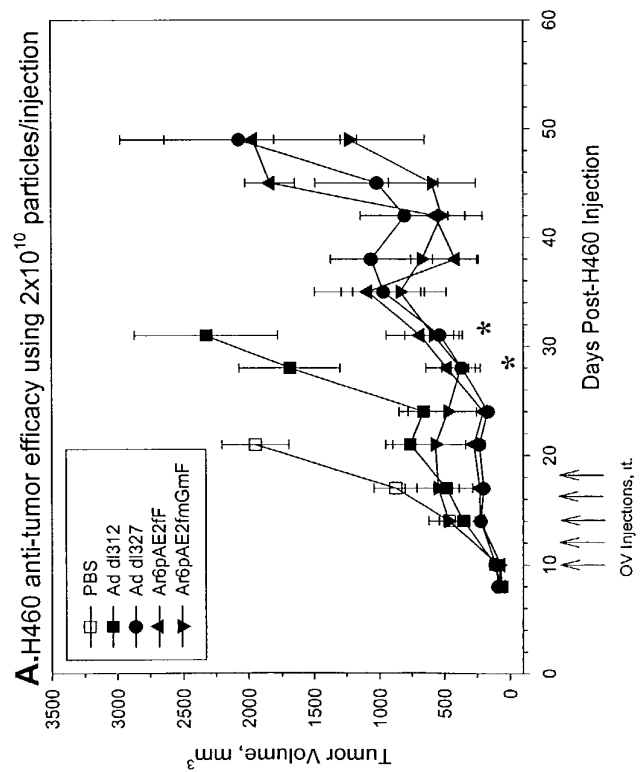


FIG. 23
A. H460 anti-tumor efficacy using 2×10^{10} particles/injection
B. H460 anti-tumor efficacy using 1×10^{11} particles/injection

FIGURE 24

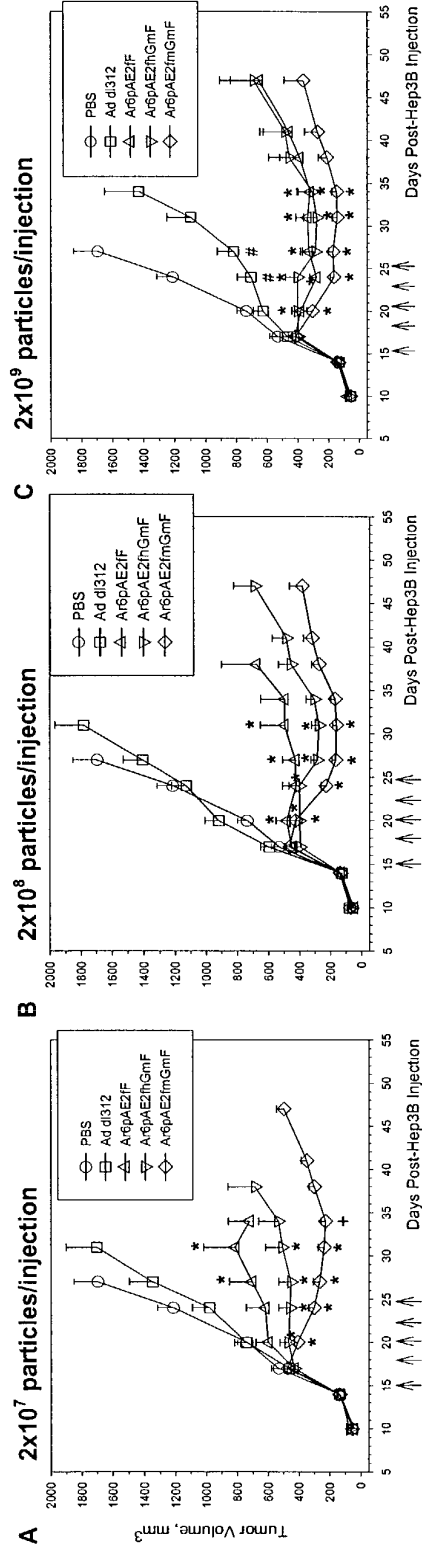


FIGURE 25

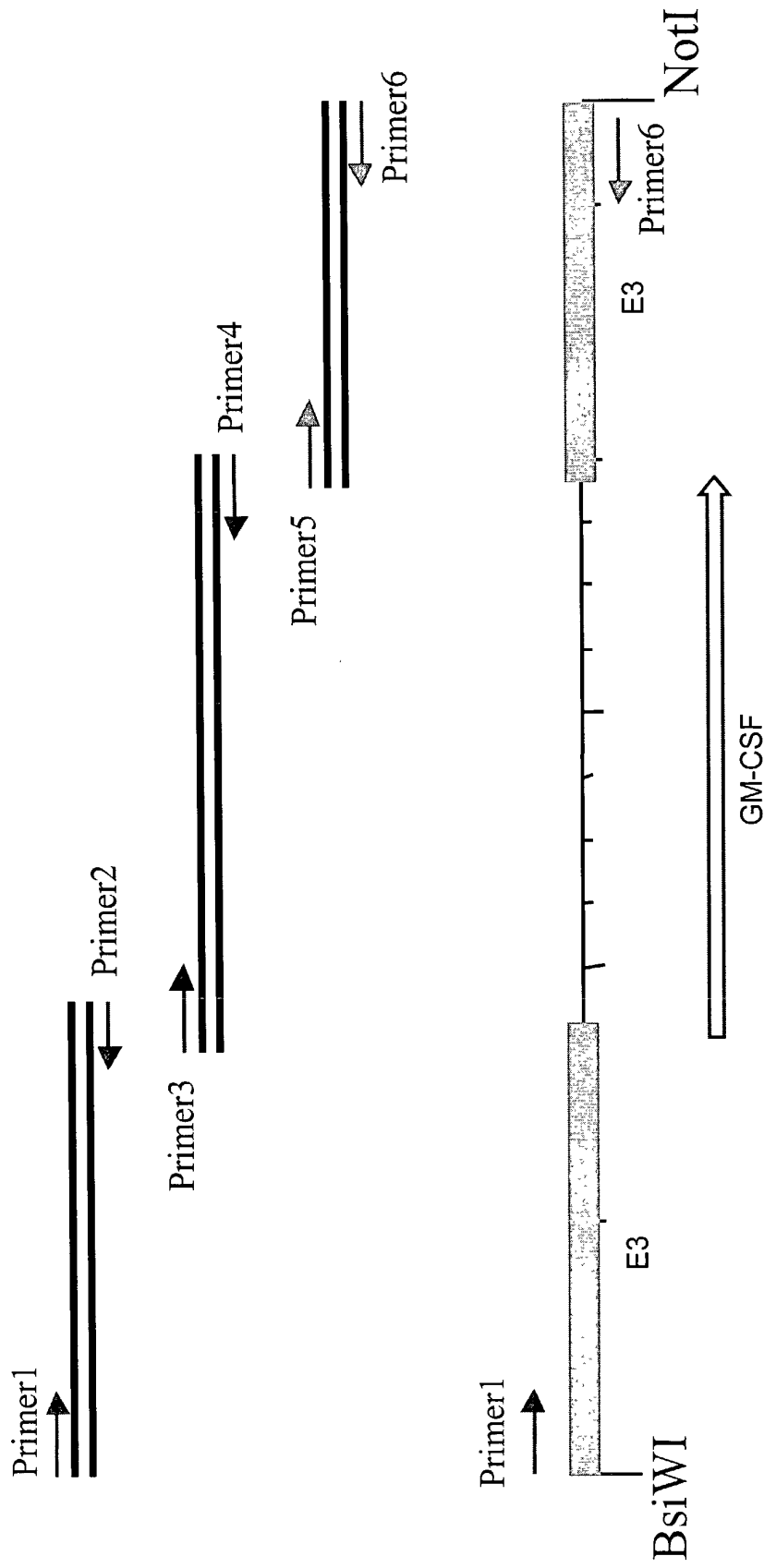


FIGURE 26A

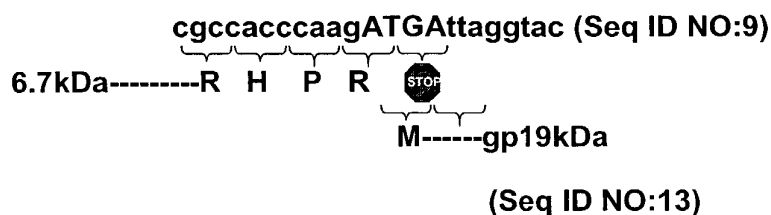


FIGURE 26B

1. Δ gp19a:

atgg

6.7kDa—plus 9aa to **STOP** M—mouse GMCSF

atgt

6.7kDa—plus 33aa to **STOP** M—human GMCSF
2. Δ gp19b: cgccaccaag ATAACCatg..... (SEQ ID NO:98)

6.7kDa—R H P R **STOP** M—GMCSF
3. Δ gp19c: cgccaccaagatgA.....(Seq ID NO:10)

6.7kDa—R H P R **STOP**

M—GMCSF
4. Δ gp19d: cgccaccaagATGACCatg.....(Seq ID NO:11)

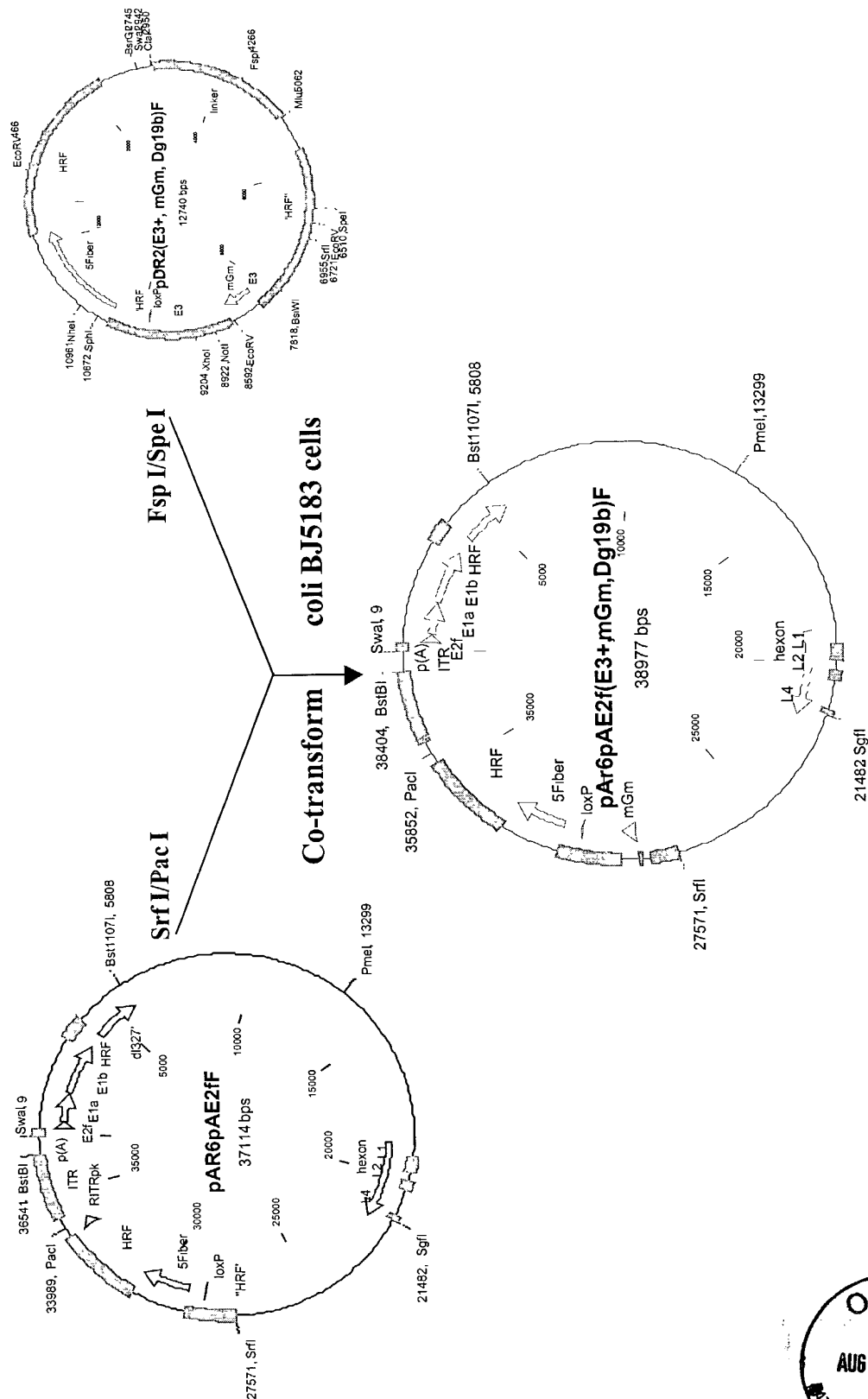
6.7kDa—R H P R **STOP**

M T M—GMCSF
5. Δ gp19b/IRES: cgccaccaagatga CAATTC...IRES...atg..... (Seq ID NO:12)

6.7kDa—R H P R **STOP** M—GMCSF



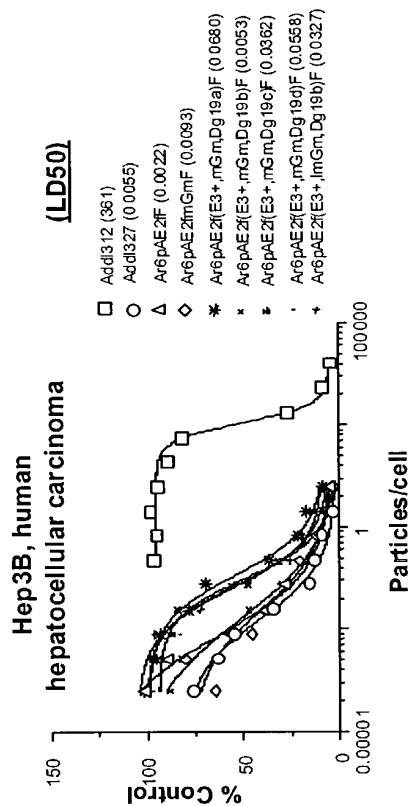
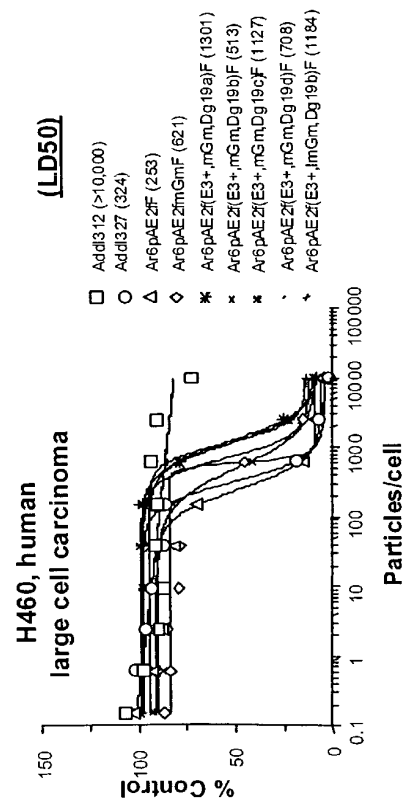
FIGURE 27A



[illegible]

FIGURE 28

A.



B.

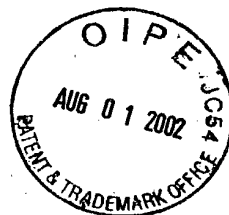
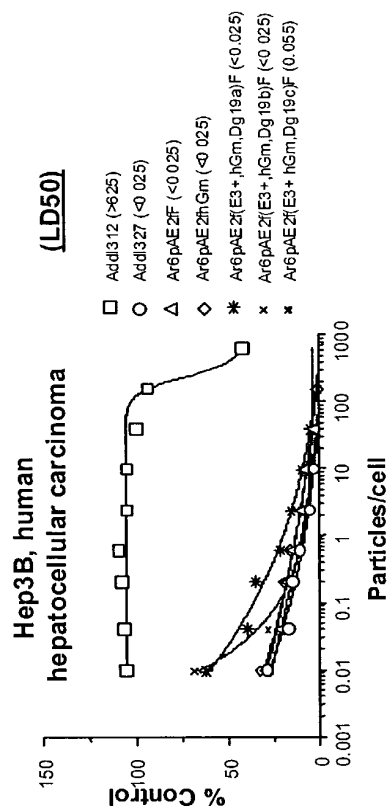
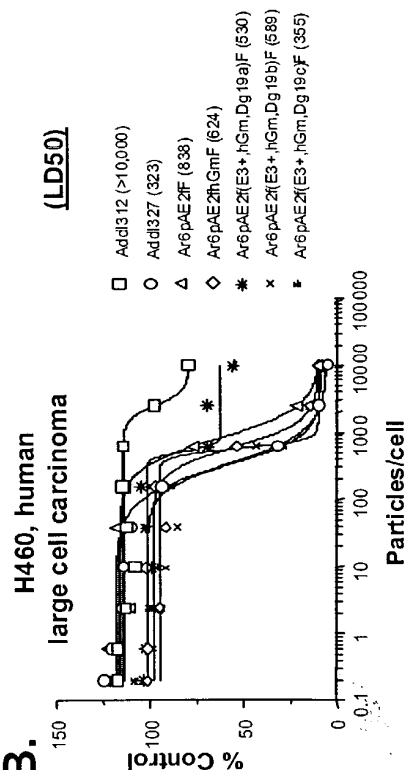
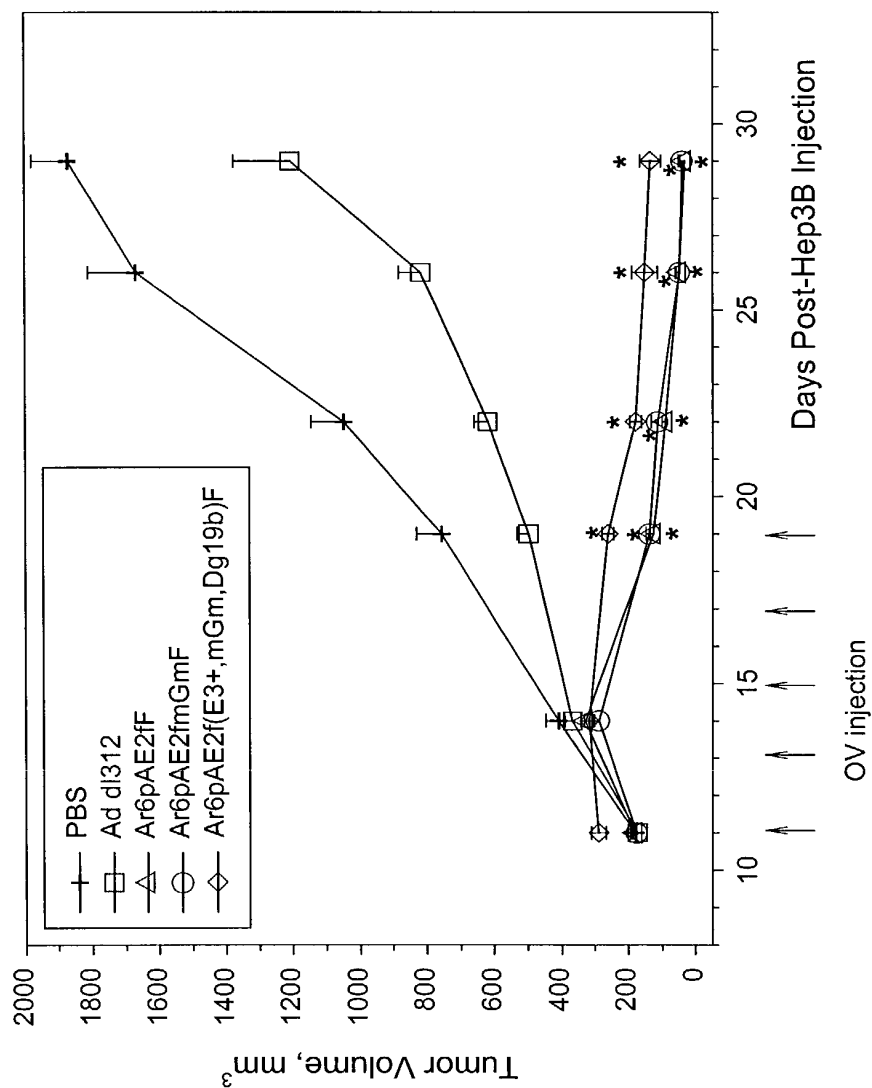




Figure 30



1000
800
600
400
200
0

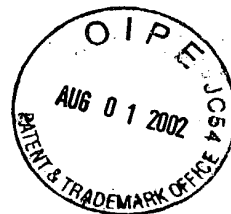


Figure 31

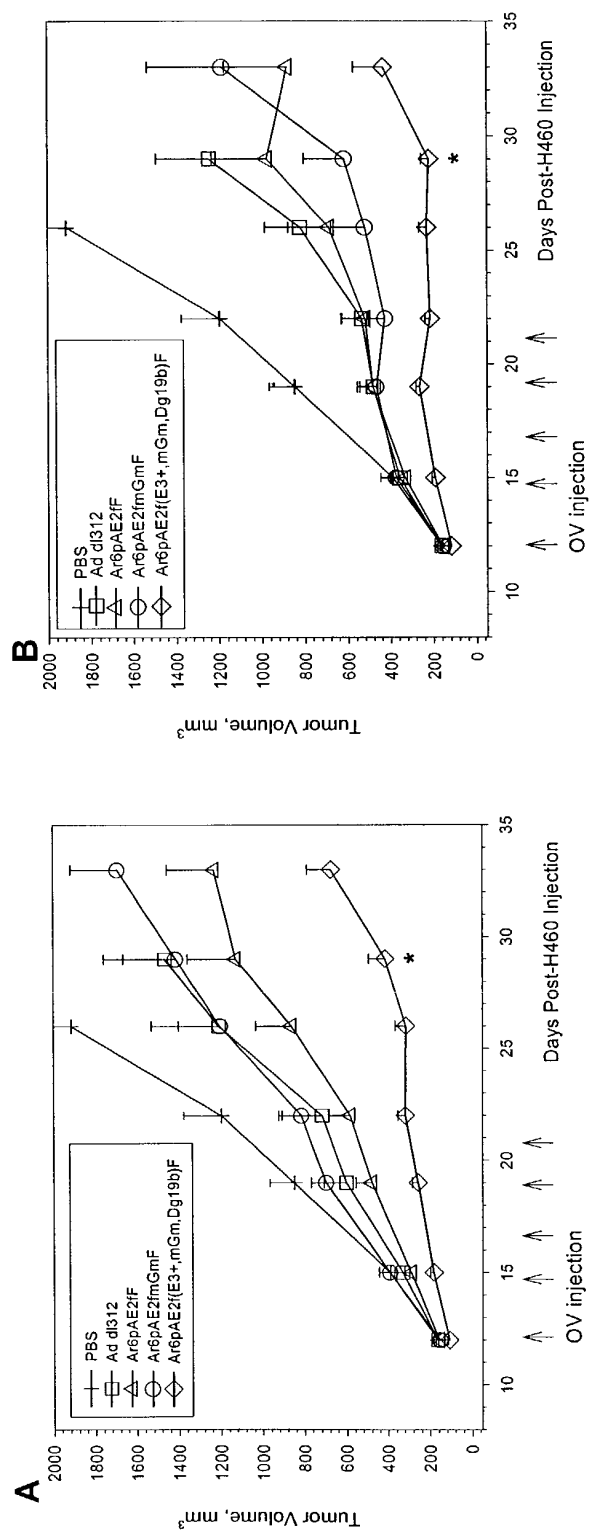
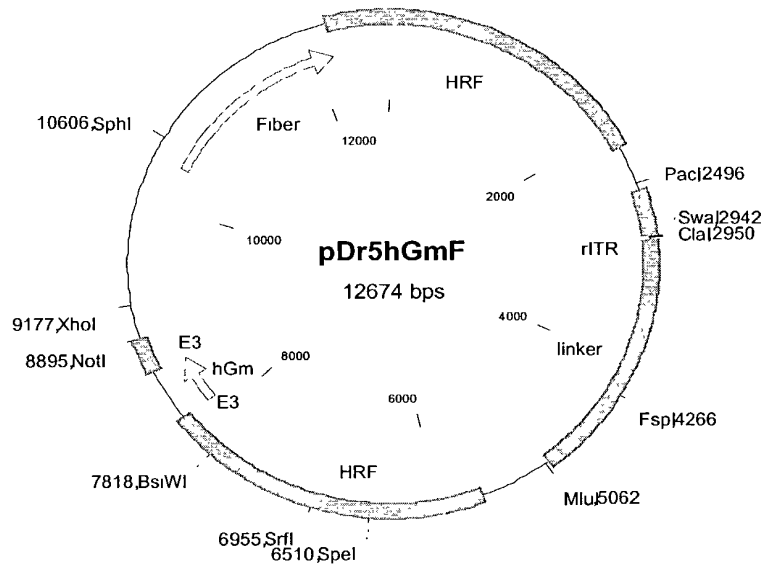


Figure 32

A. pDr5hGmF



B. pDr5mGmF

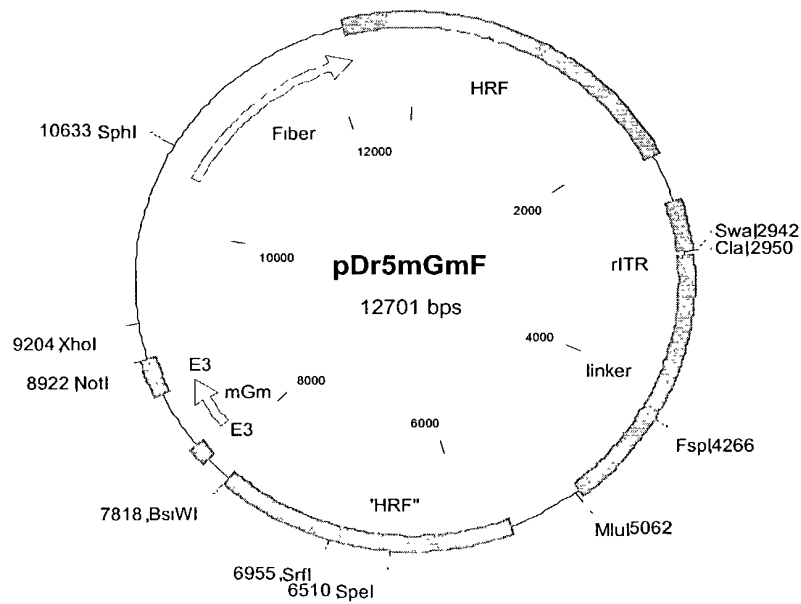


Figure 33

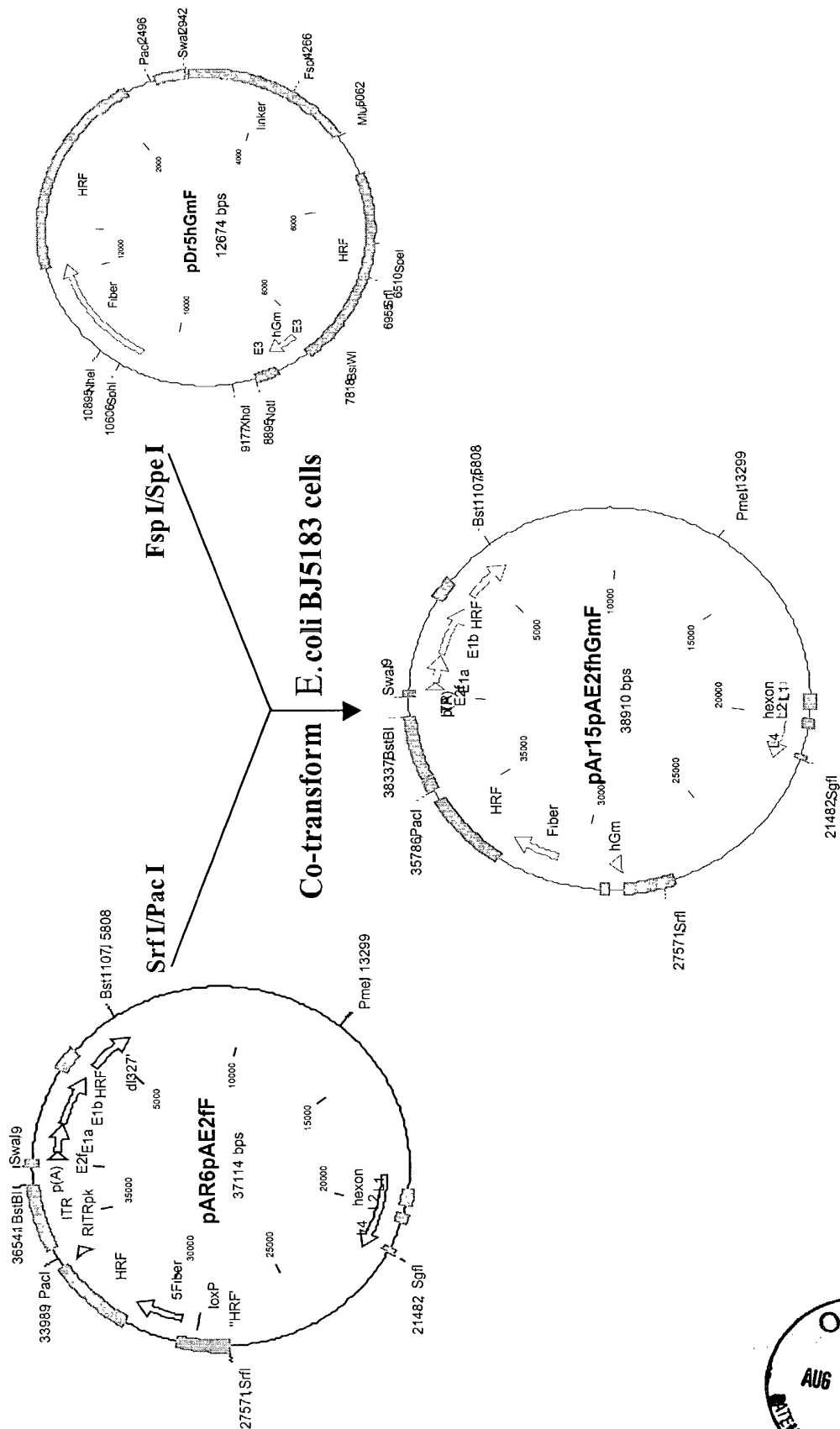


Figure 34

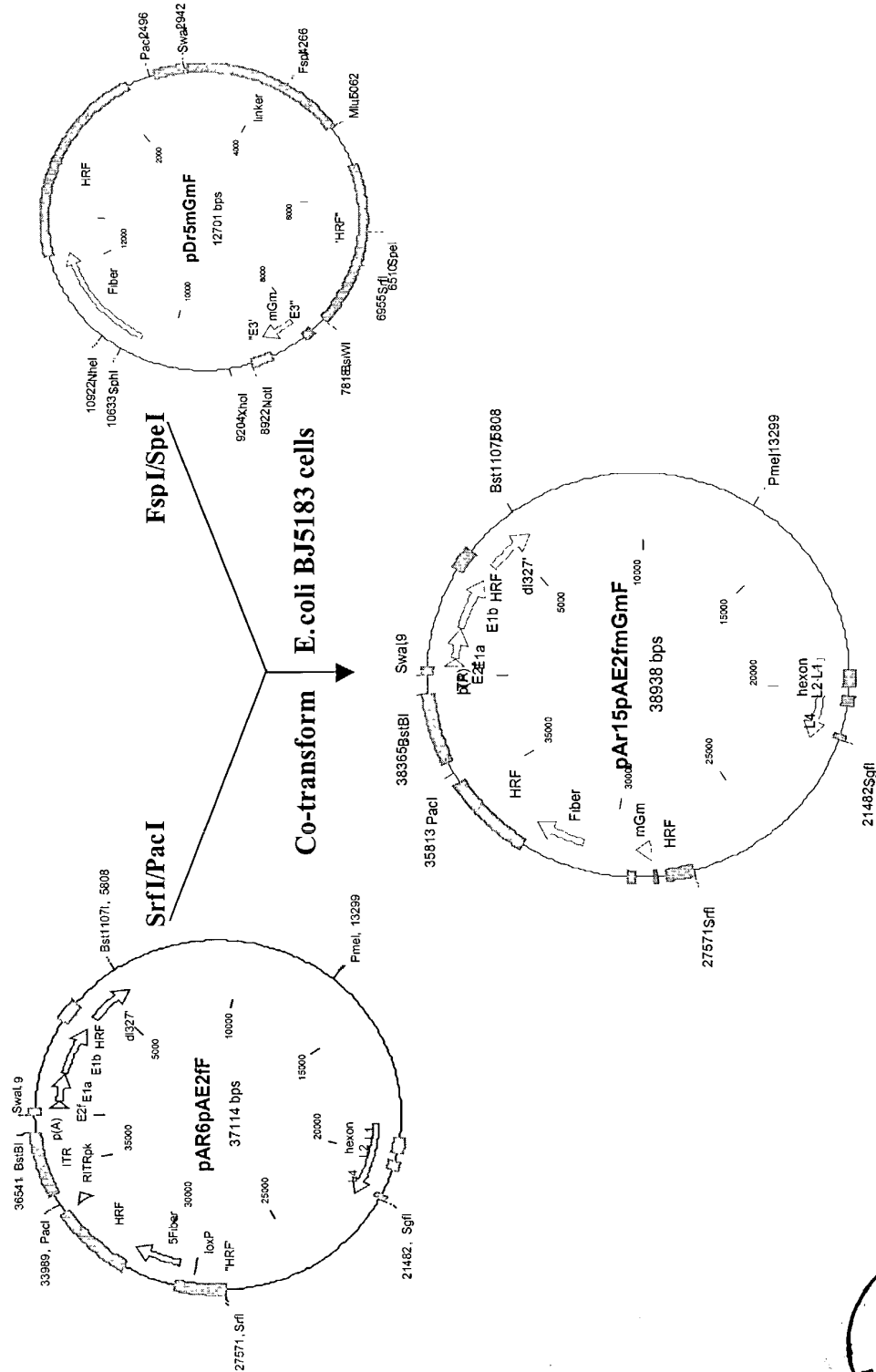


Figure 35

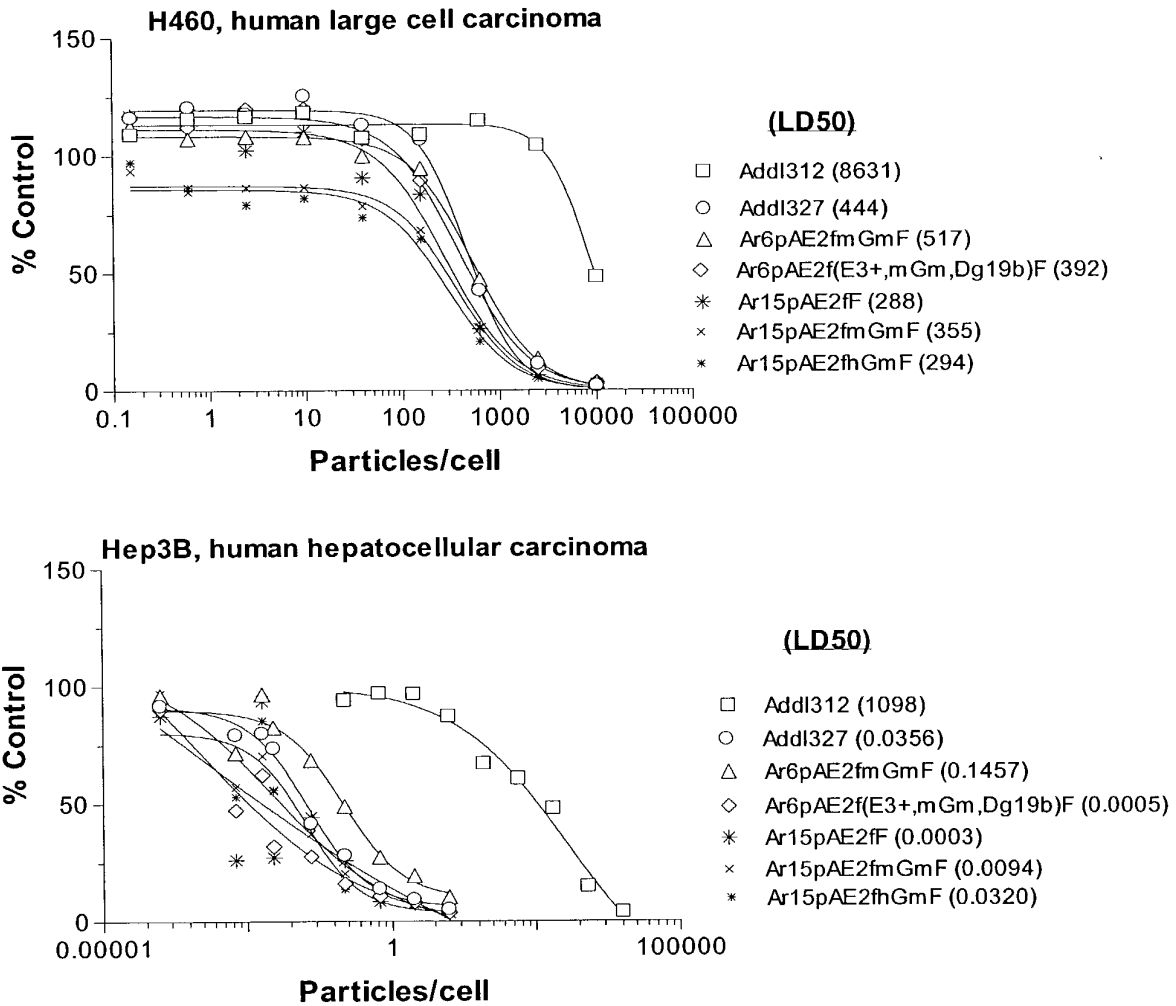


Figure 36

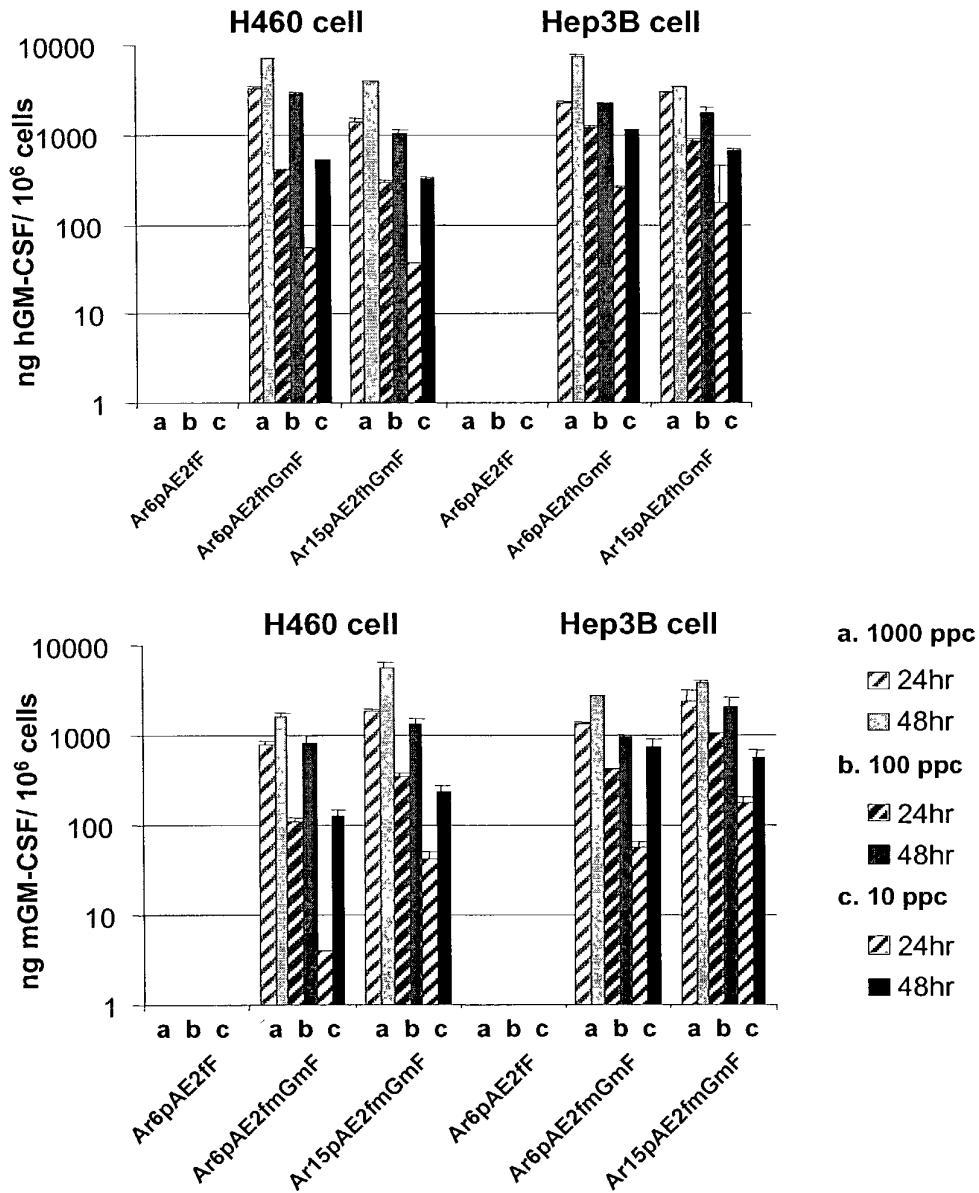
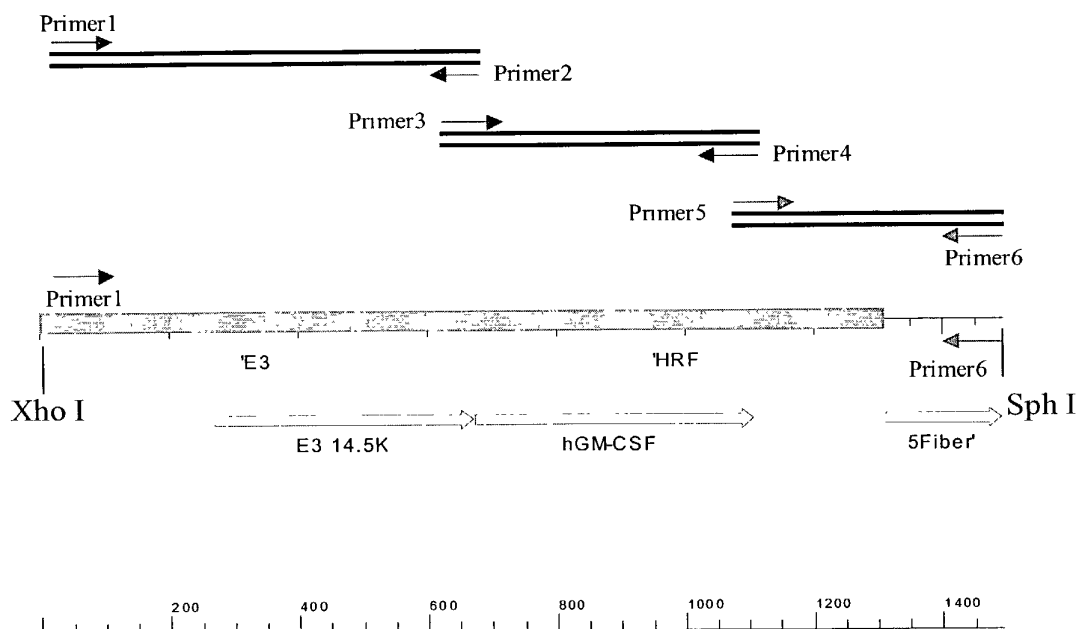


Figure 37



E3-hGm/XhoI + SphI (1491 bps)



Figure 38A

ggaggagATGacTGAtttaggtac (Seq ID NO:14)
E3 14.5kDa-----G G D D STOP (Seq ID NO:16)
M-----E3 14.7kDa

Figure 38B

ggaggagacgacTGACC atg,..... (Seq ID NO:15)
E3 14.5kDa-----G G D D STOP M-----GMCSF



Figure 39

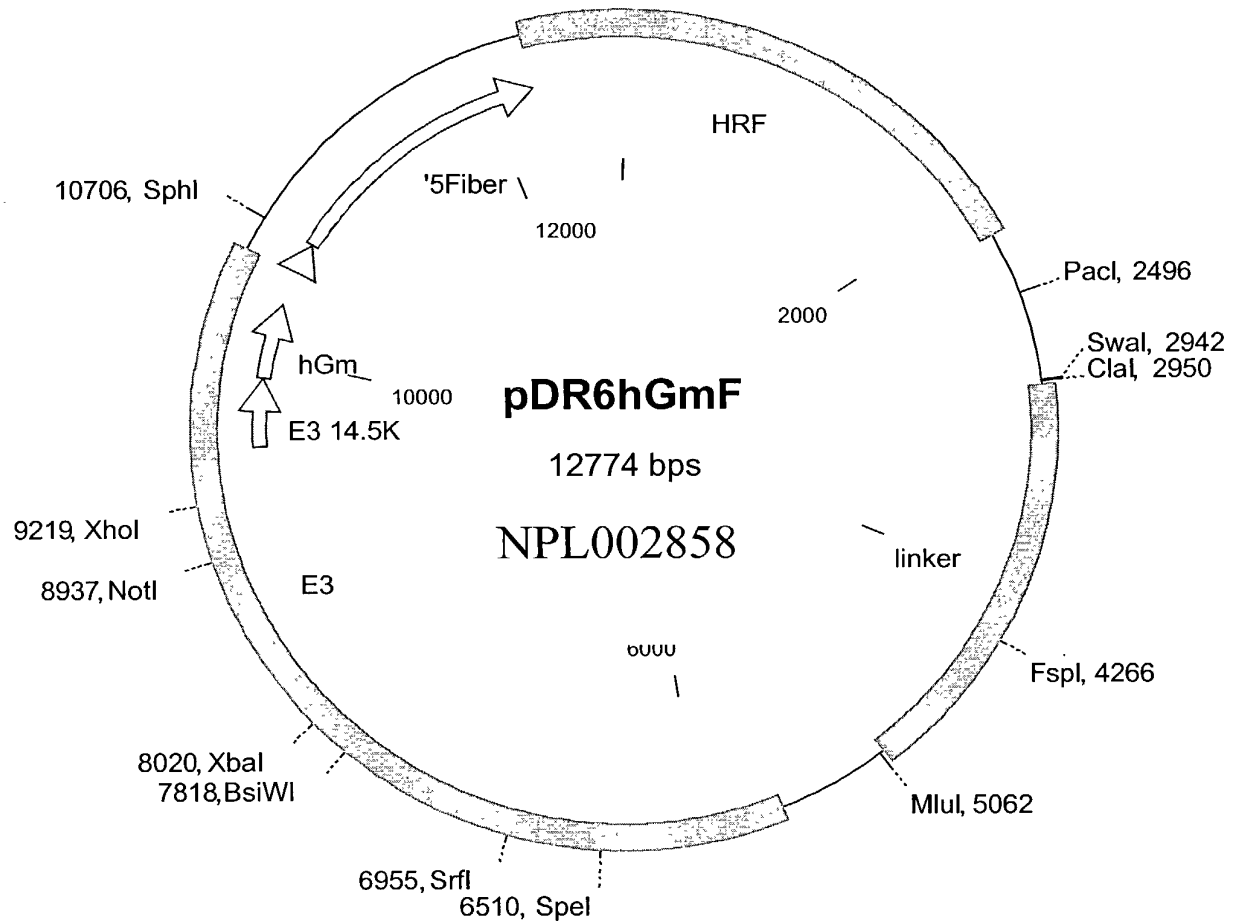
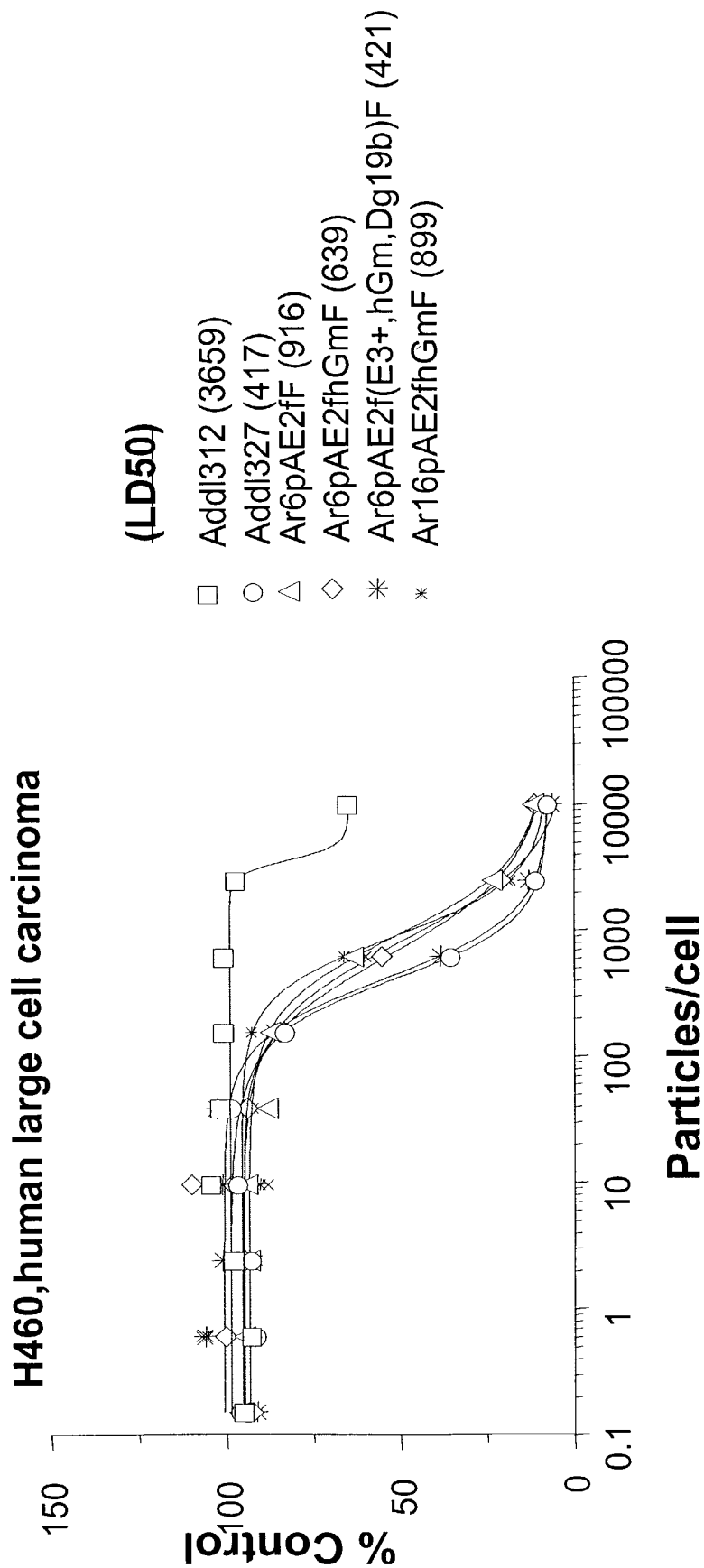


Figure 41



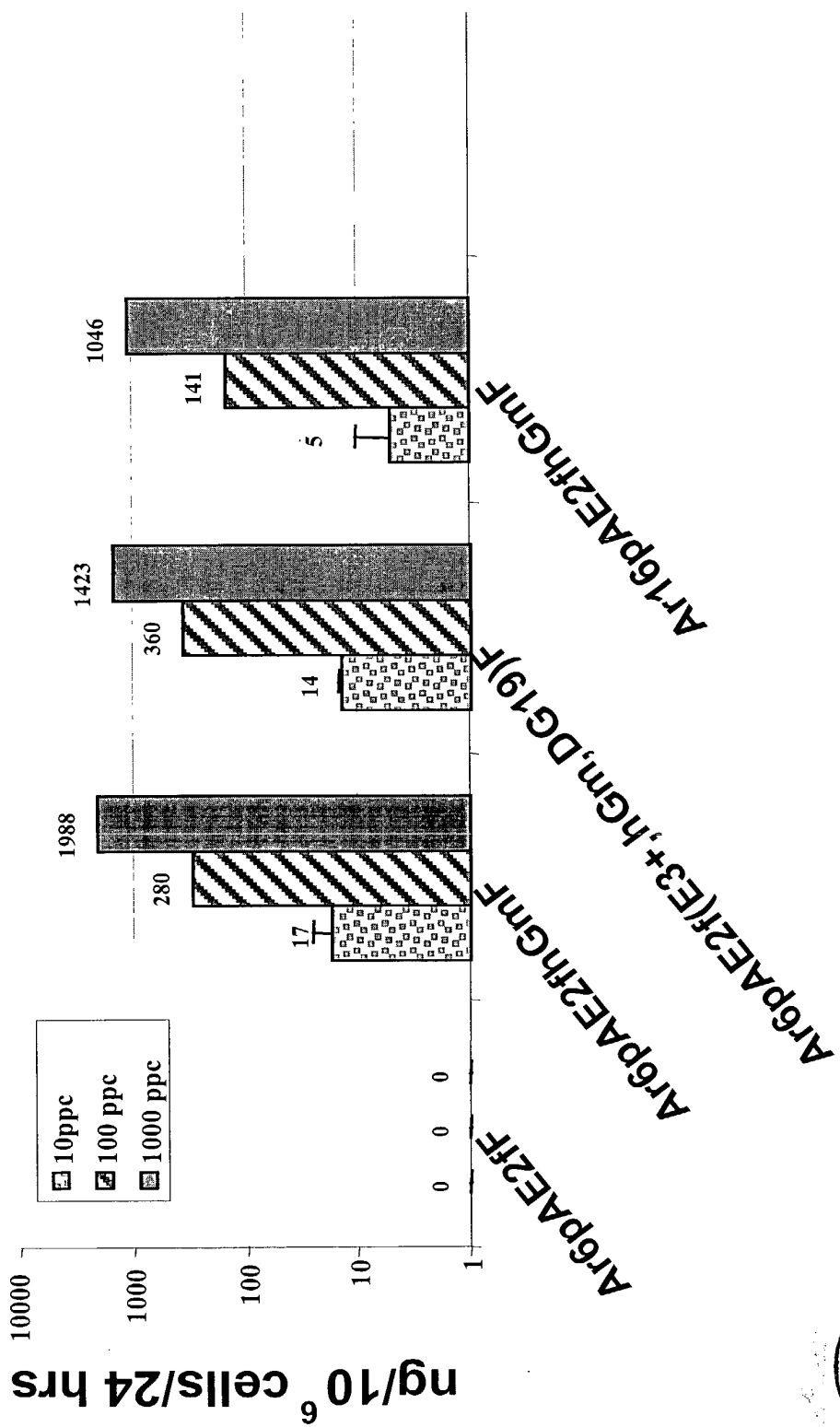
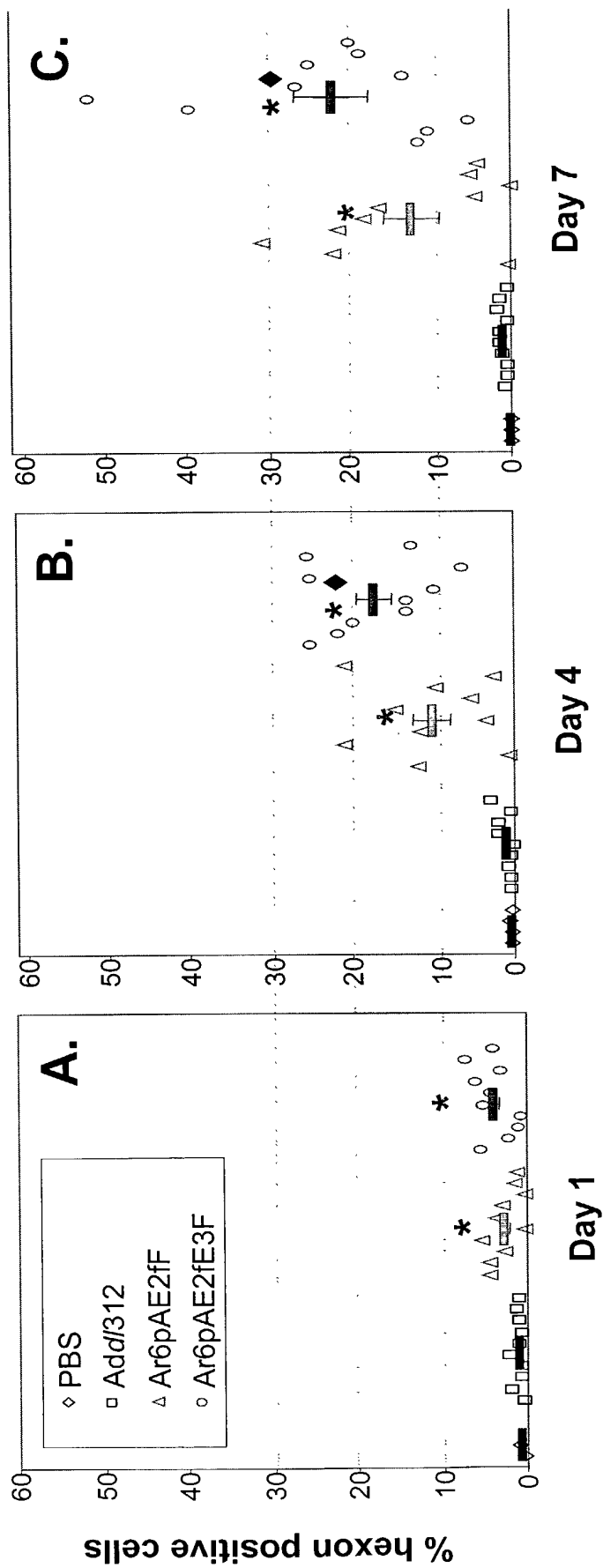


Figure 42



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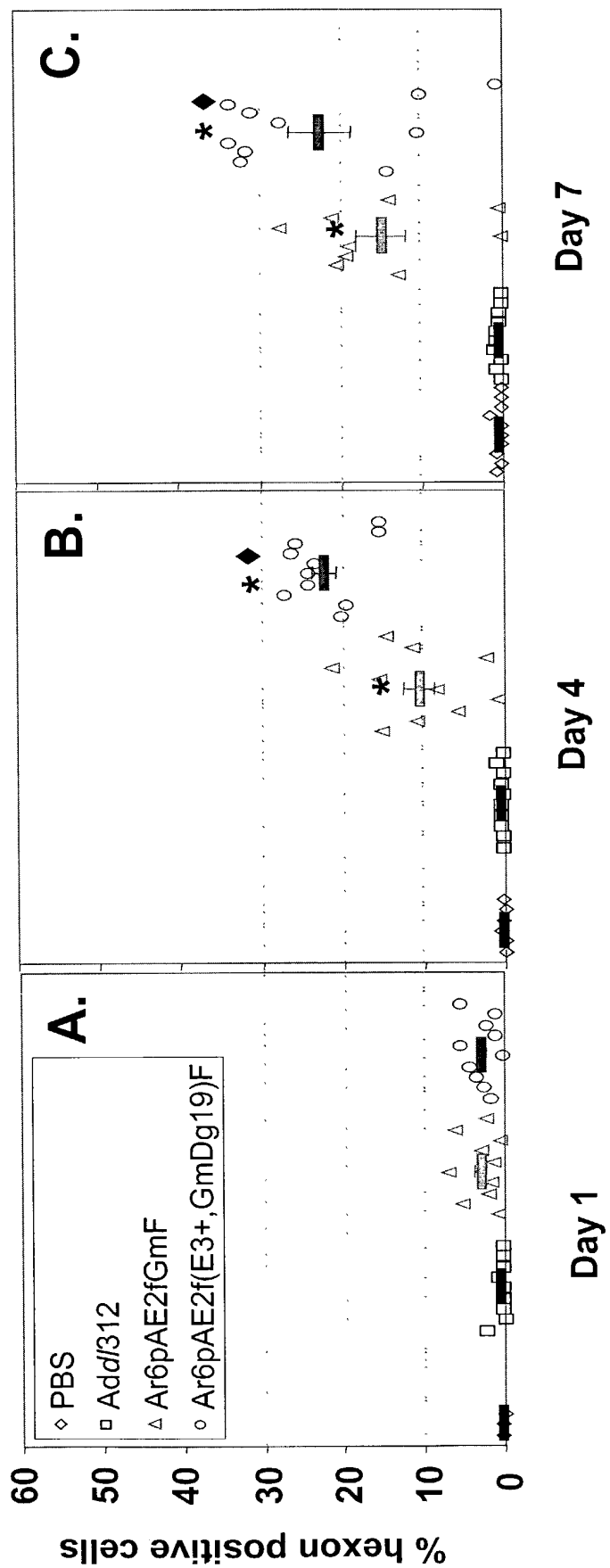
Figure 43



*: p < 0.05 between Ar6pAE2fF and Ar6pAE2fE3F and Add/312, ANOVA
 *: p < 0.05 between Ar6pAE2fF and Ar6pAE2fE3F vectors, ANOVA



Figure 44

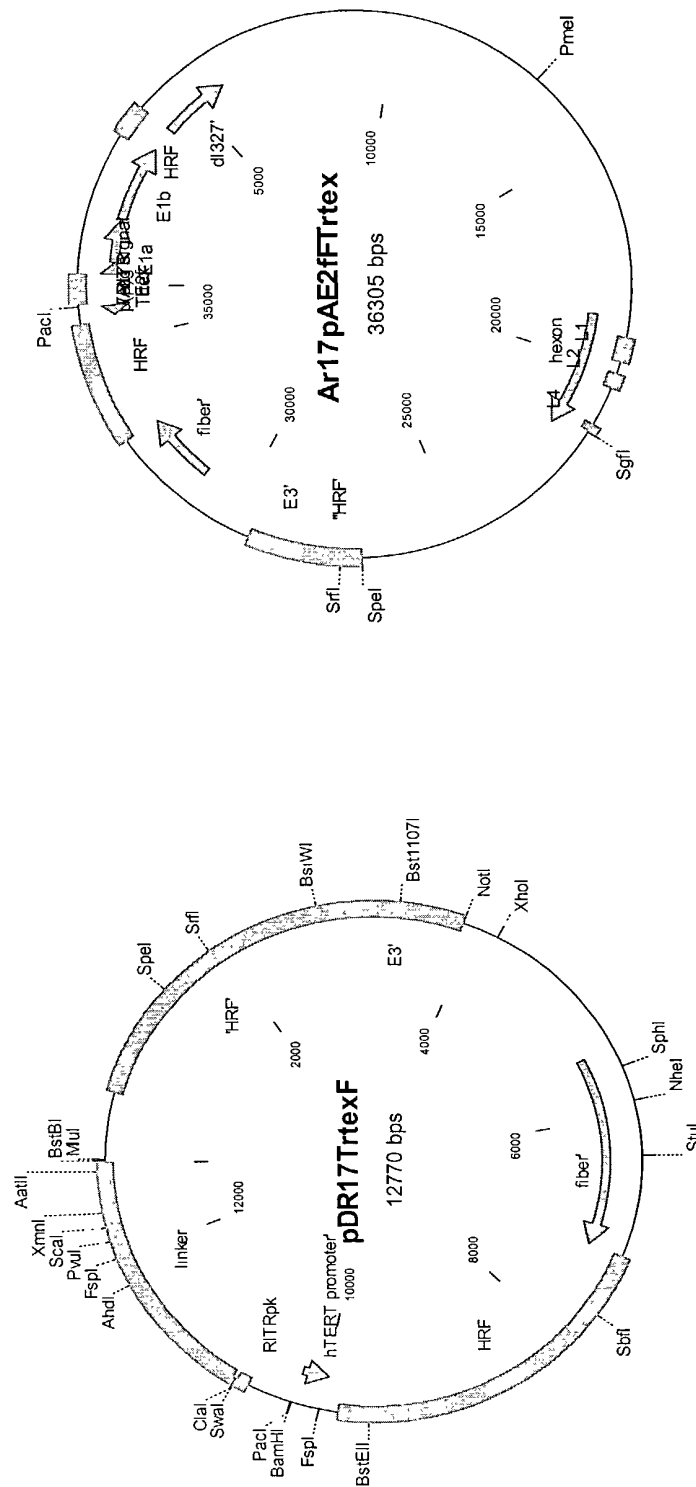


*: $p < 0.05$ between Ar6pAE2fGmF or Ar6pAE2f(E3+, hGm, Dg19)F and Add/312, ANOVA
 •: $p < 0.05$ between Ar6pAE2fGmF and Ar6pAE2f(E3+, hGm, Dg19)F vectors, ANOVA



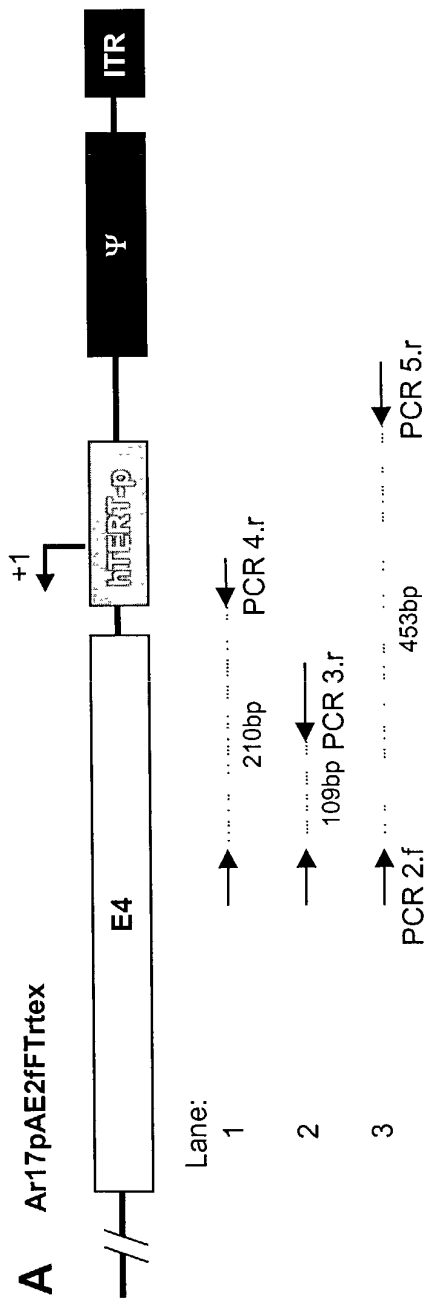
[illegible]

Figure 46



10000 15000 20000 25000 30000 35000 40000 45000 50000 55000 60000 65000 70000 75000 80000 85000 90000 95000 100000

Figure 49



[illegible]

Figure 51

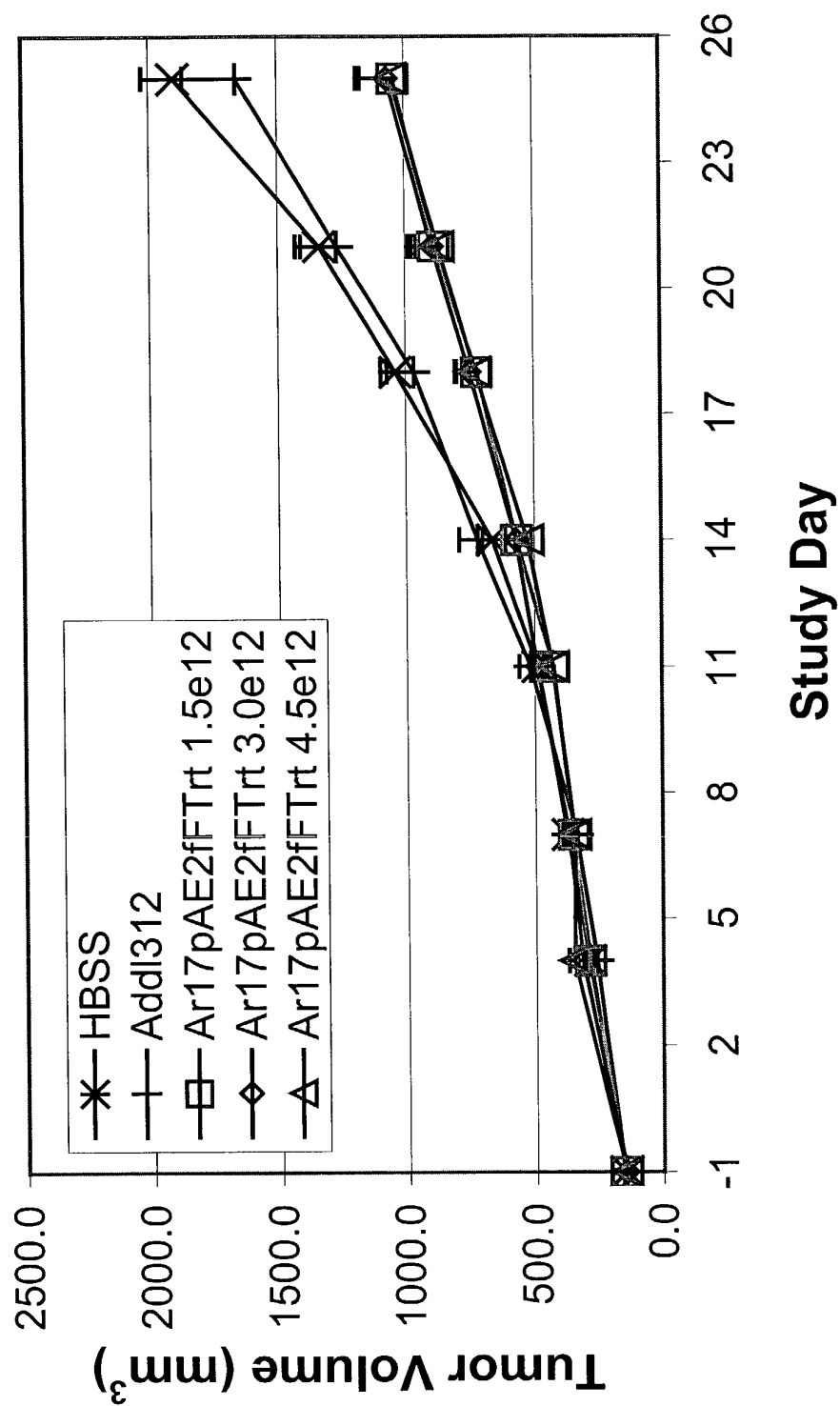


Figure 52

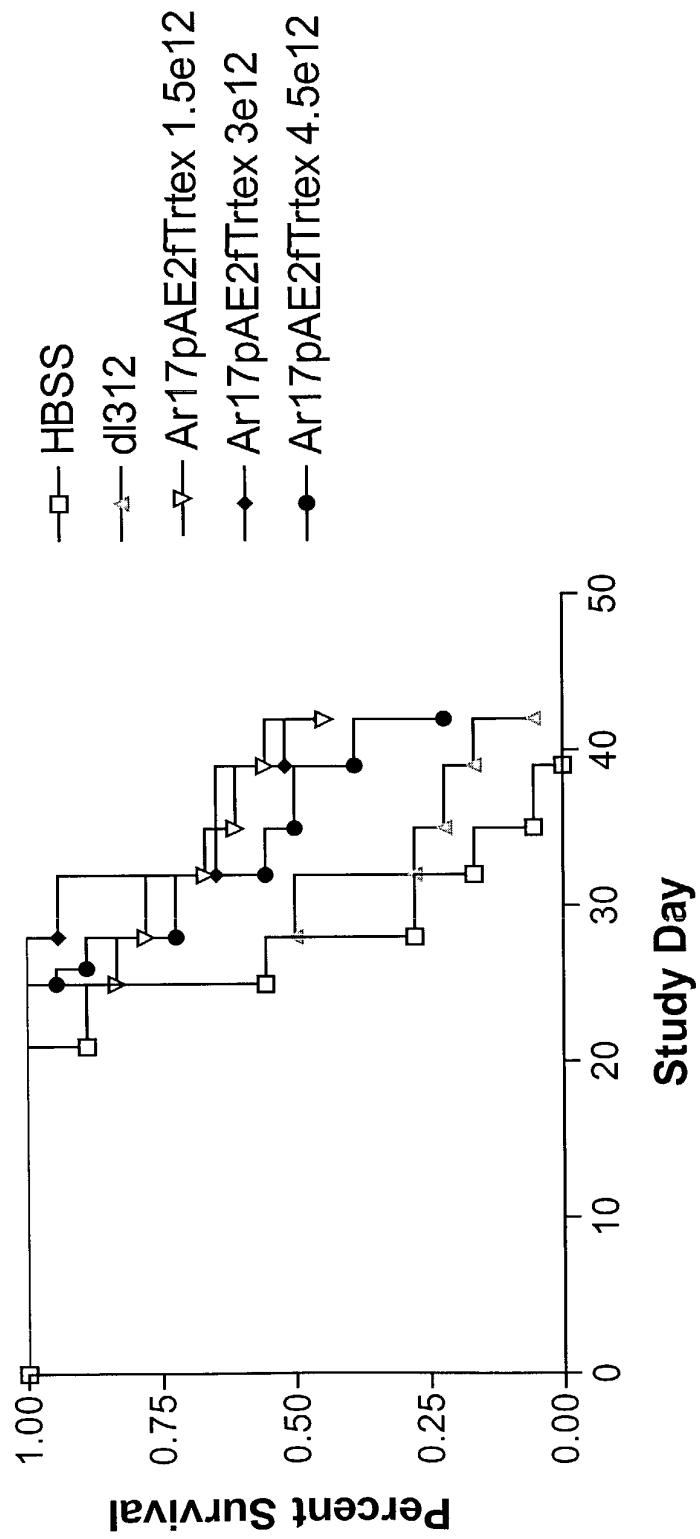


Figure 53

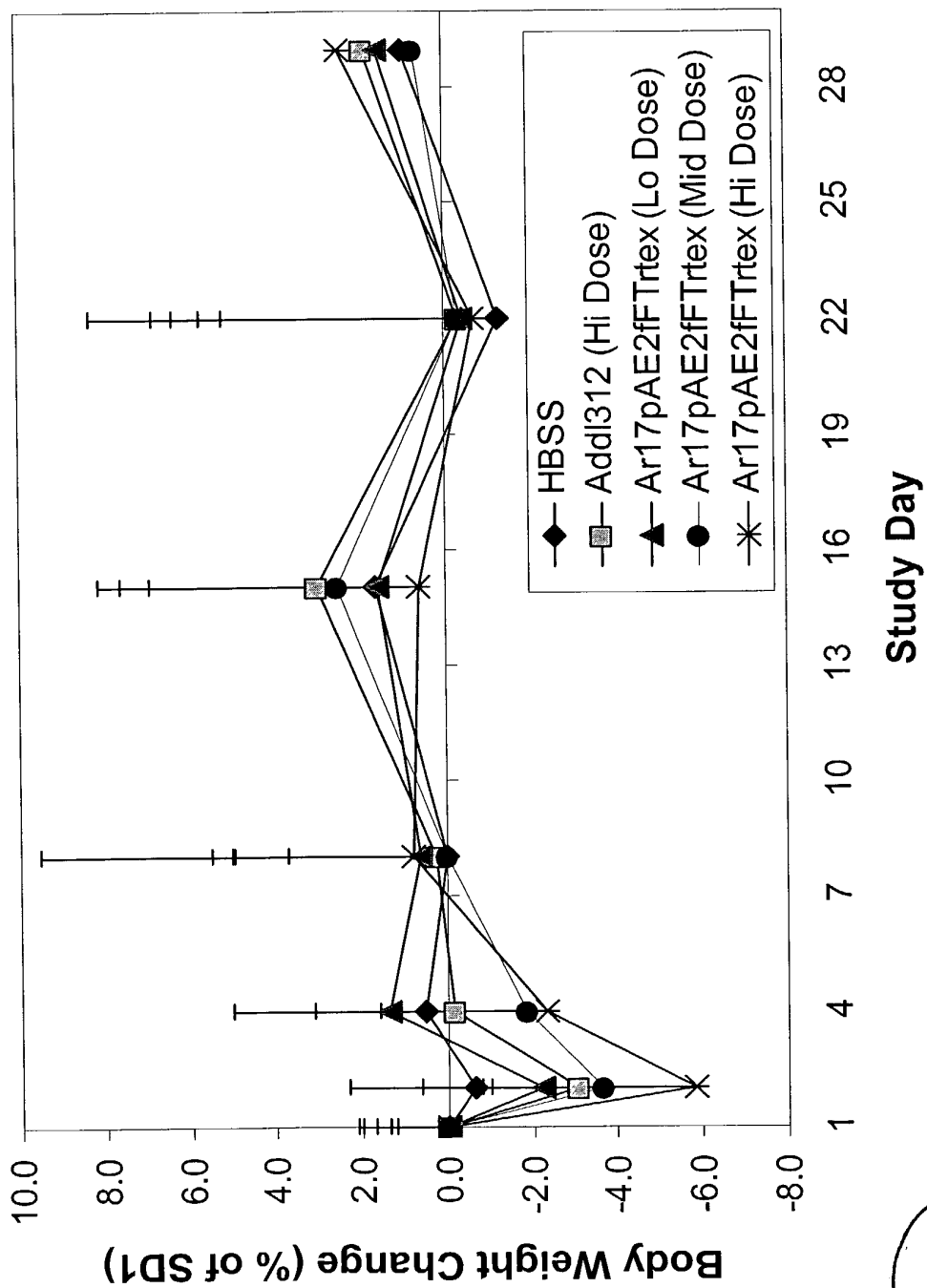
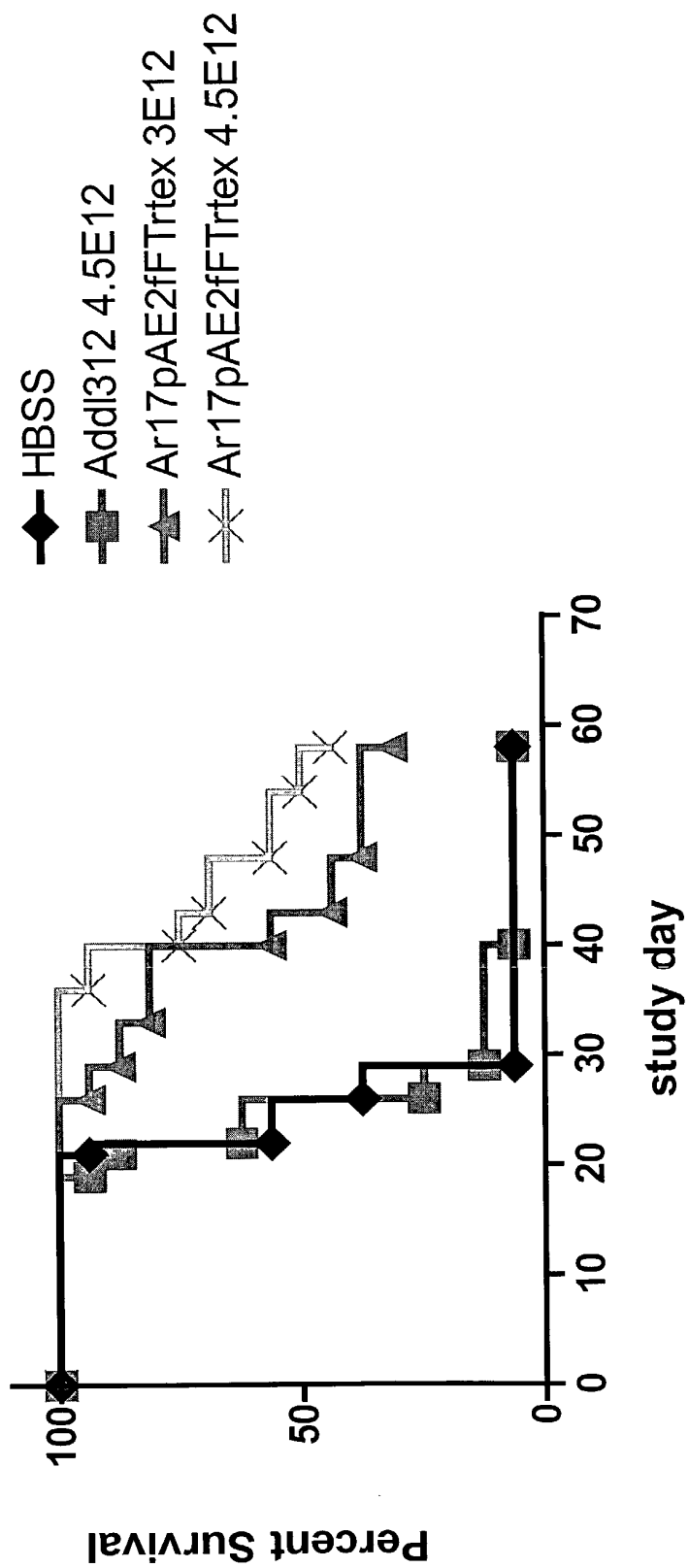


Figure 1 is a line graph showing the mean tumor volume (mm³) over 40 study days for four groups of mice. The groups are HBSS (solid line with solid circles), Addl312 4.5E12 p/kg (solid line with solid squares), Ar17pAE2fTrtex 3E12 p/kg (dashed line with open triangles), and Ar17pAE2fTrtex 4.5E12 p/kg (dashed line with crosses). The HBSS group shows the highest tumor volume, while the other three groups show significantly lower volumes, with the 4.5E12 p/kg groups showing the lowest volumes. Asterisks indicate statistical significance.

Study day	HBSS (mm³)	Addl312 4.5E12 p/kg (mm³)	Ar17pAE2fTrtex 3E12 p/kg (mm³)	Ar17pAE2fTrtex 4.5E12 p/kg (mm³)
0	~150	~150	~150	~150
5	~350	~300	~300	~300
10	~550	~400	~400	~400
15	~850	~500	~500	~500
20	~1200	~600	~600	~600
25	~1350	~700	~700	~700
30	~1400	~800	~800	~800
35	~1400	~900	~900	~900
40	~1400	~1000	~1000	~1000

$$-\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) + \frac{\partial L}{\partial x} = 0, \quad \text{for } x \in \mathbb{R}^n.$$

Figure 55



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[illegible]

Figure 58

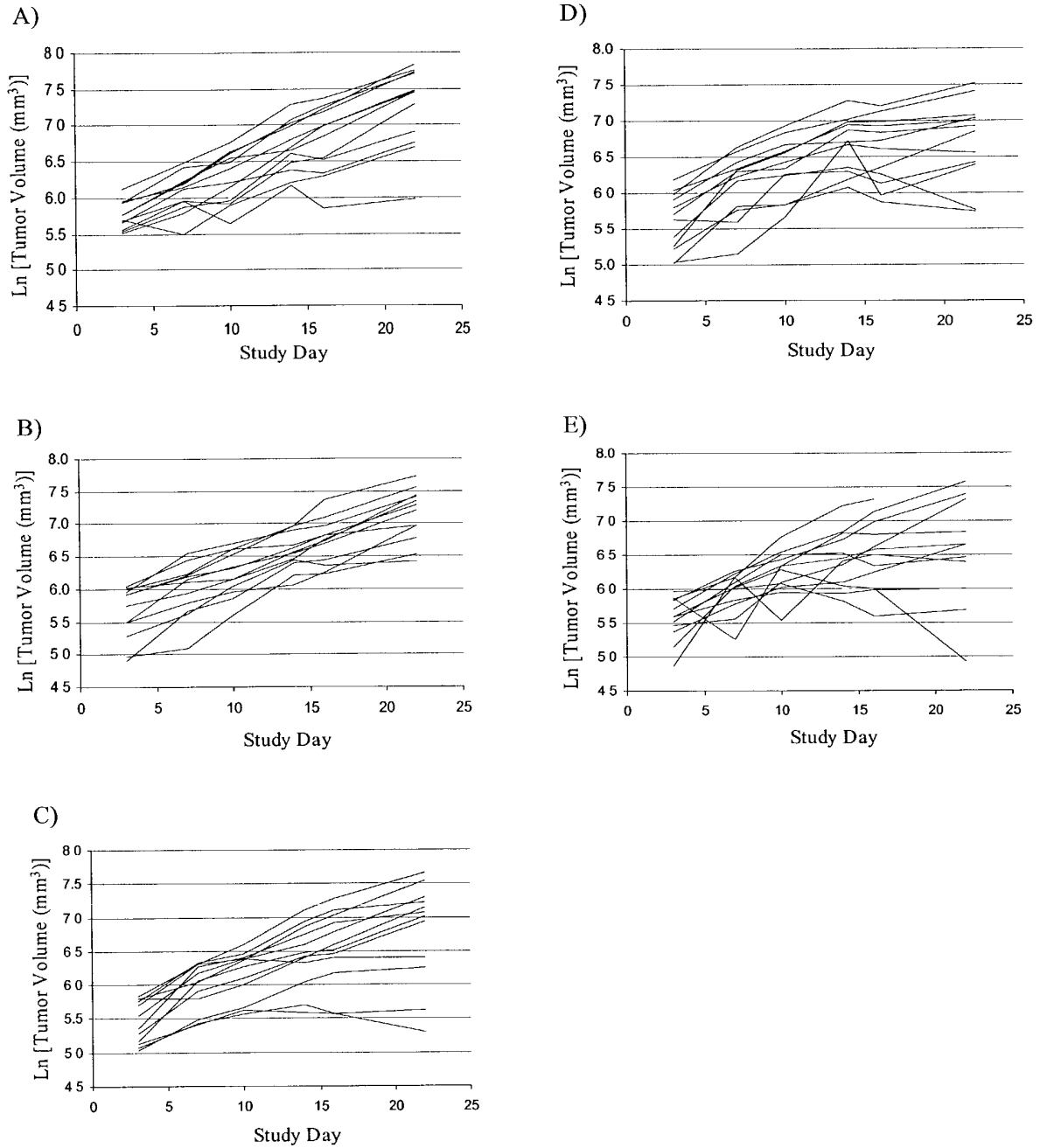


Figure 59

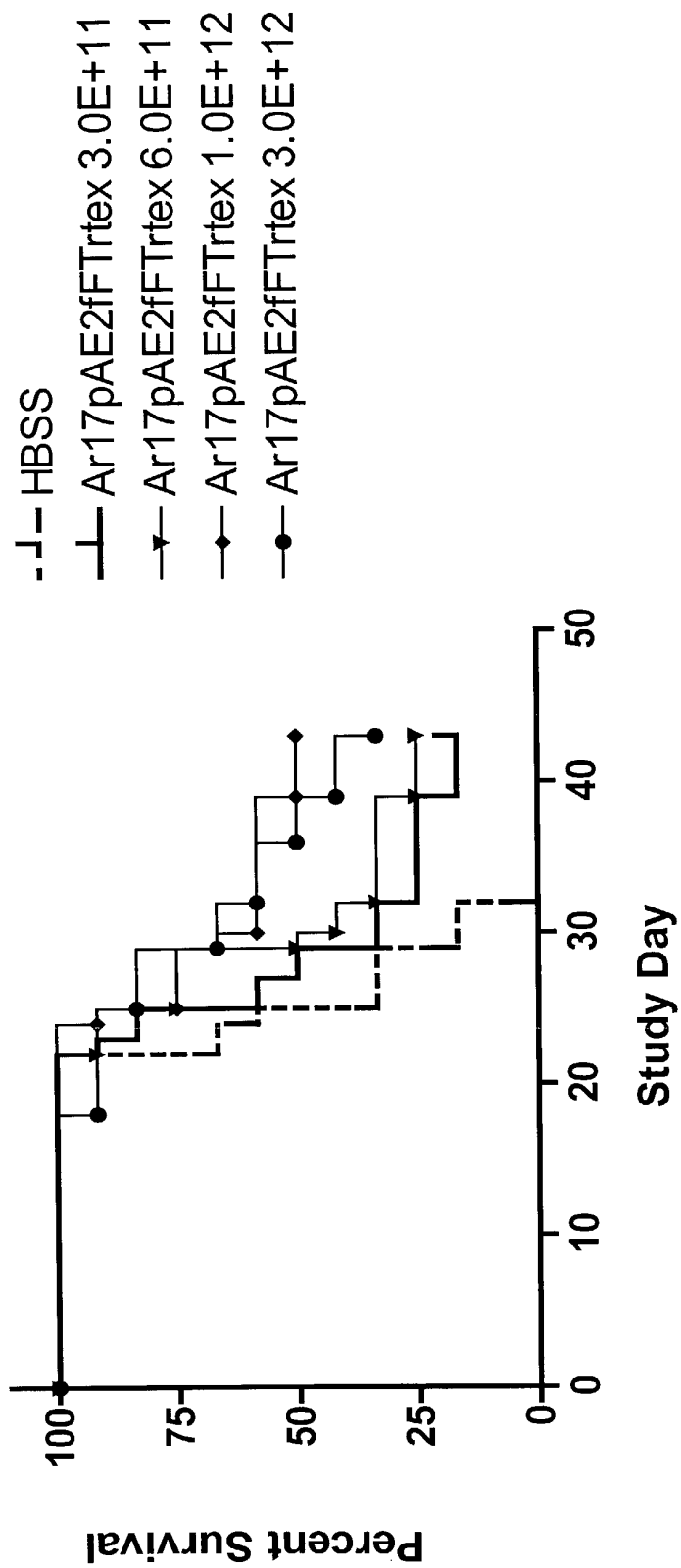
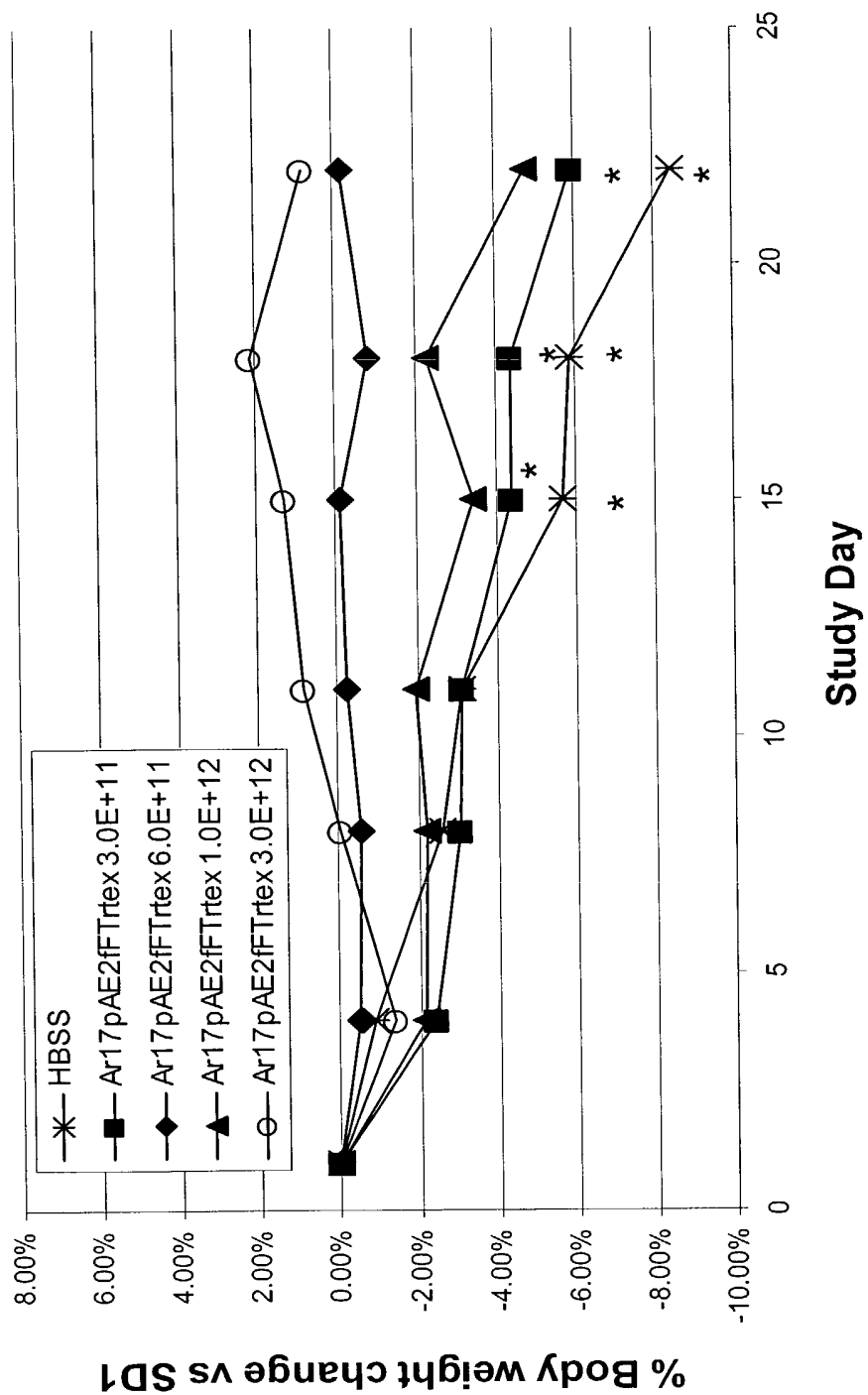


Figure 60



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Figure 61

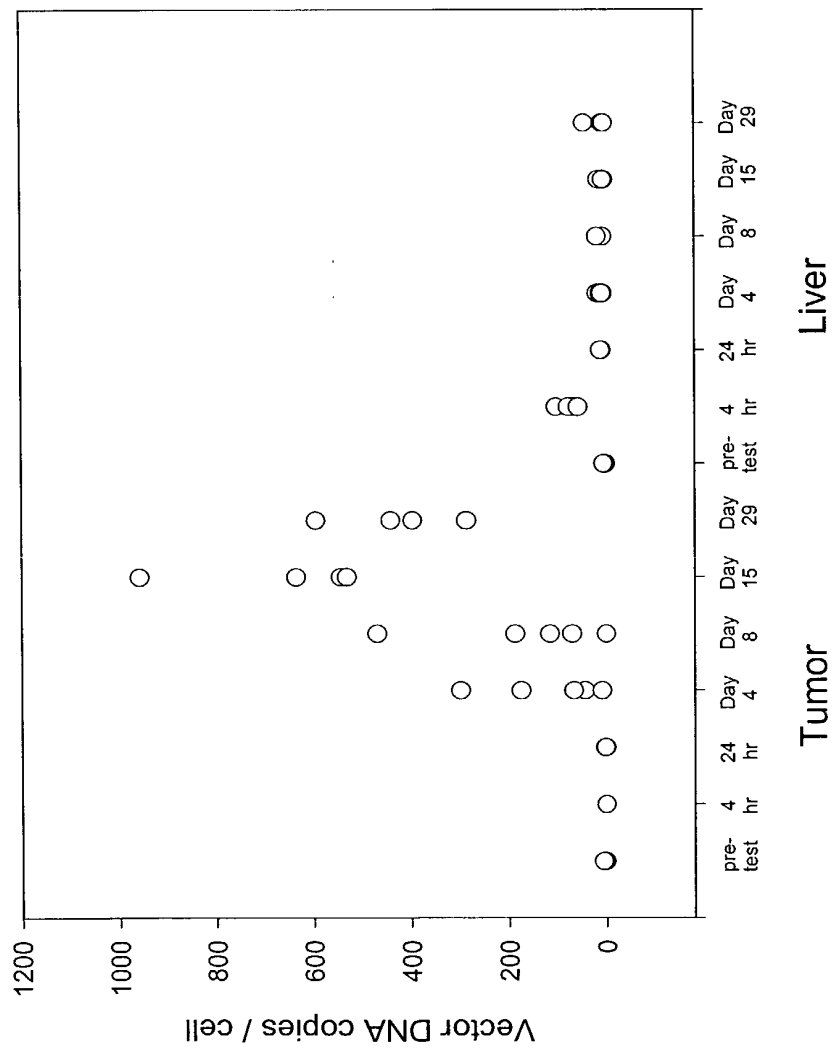


Figure 62

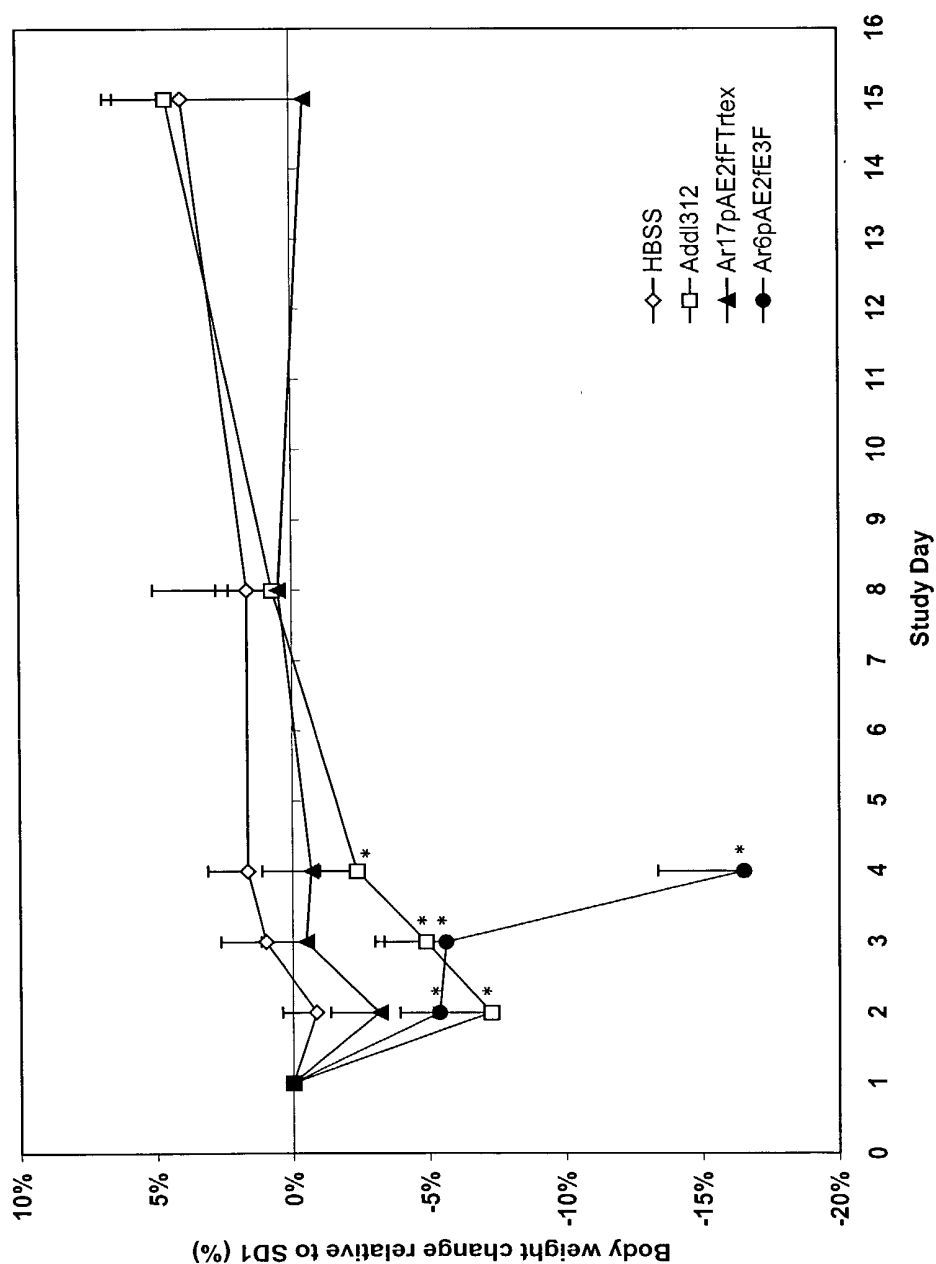


FIGURE 63

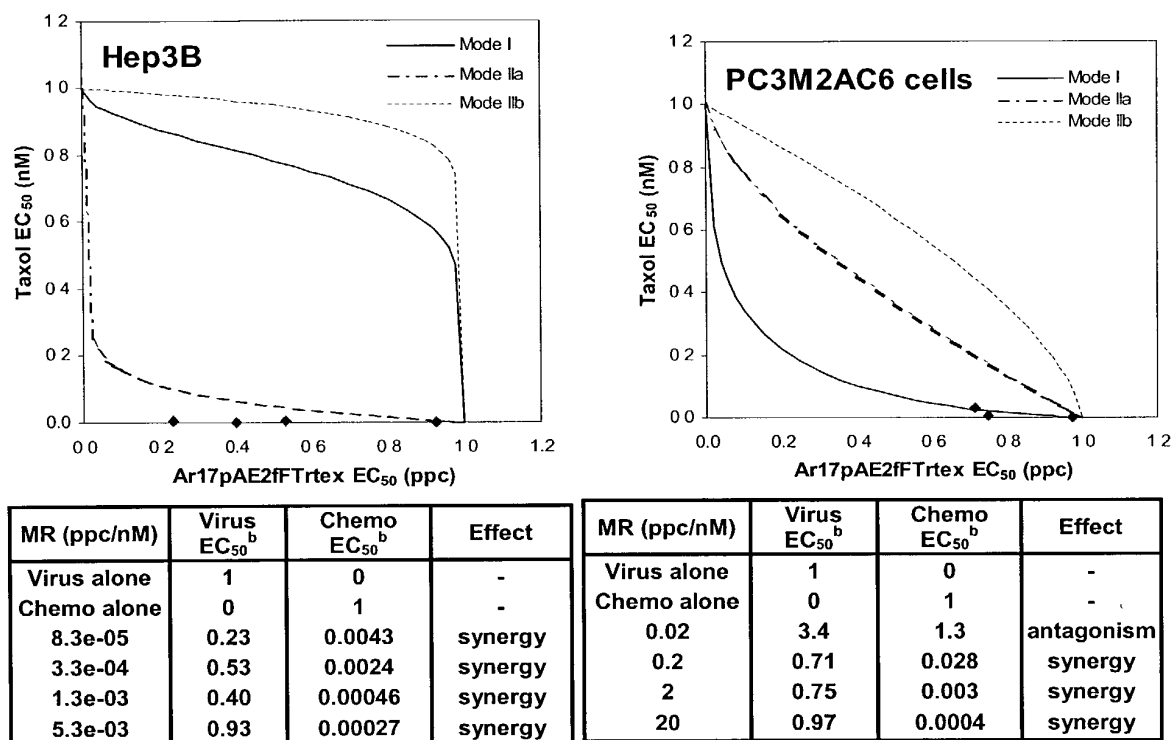
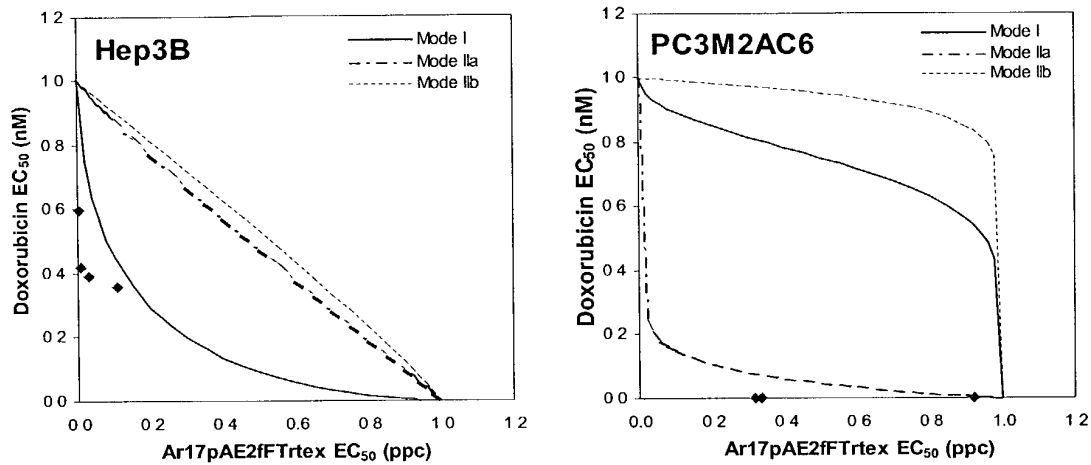


Figure 64

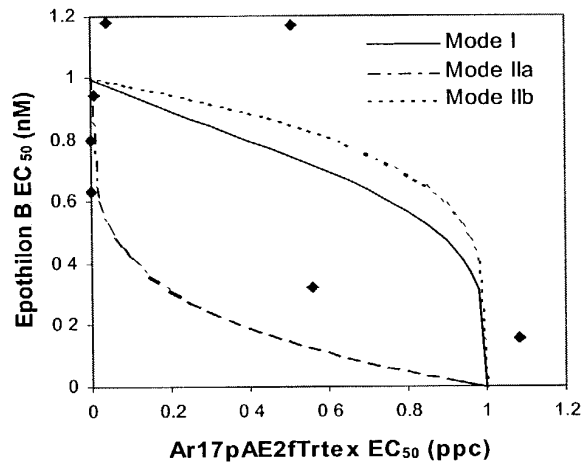


MR (ppc/nM)	Virus EC ₅₀ ^b	Chemo EC ₅₀ ^b	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
1.3e-05	0.0028	0.60	synergy
5.0e-05	0.0078	0.42	synergy
2.0e-04	0.029	0.39	synergy
8.0e-04	0.11	0.36	synergy

MR (ppc/nM)	Virus EC ₅₀ ^b	Chemo EC ₅₀ ^b	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
1	2.2	0.015	antagonism
10	0.92	6.1e-4	synergy
100	0.34	2.2e-5	synergy
1000	0.32	2.1e-6	synergy



Figure 65



	Virus EC ₅₀ ^b	Chemo EC ₅₀ ^b	Effect
Virus alone	1	0	-
Chemo alone	0	1	-
3.1e-06	0.00045	0.63	synergy
1.3e-05	0.0018	0.80	synergy
5.0e-05	0.0084	0.95	synergy
2.0e-04	0.042	1.2	antagonism
8.0e-04	0.18	1.6	antagonism
3.2e-03	0.51	1.2	antagonism
1.3e-02	0.56	0.32	additivity
5.1e-02	1.1	0.06	antagonism



Figure 66

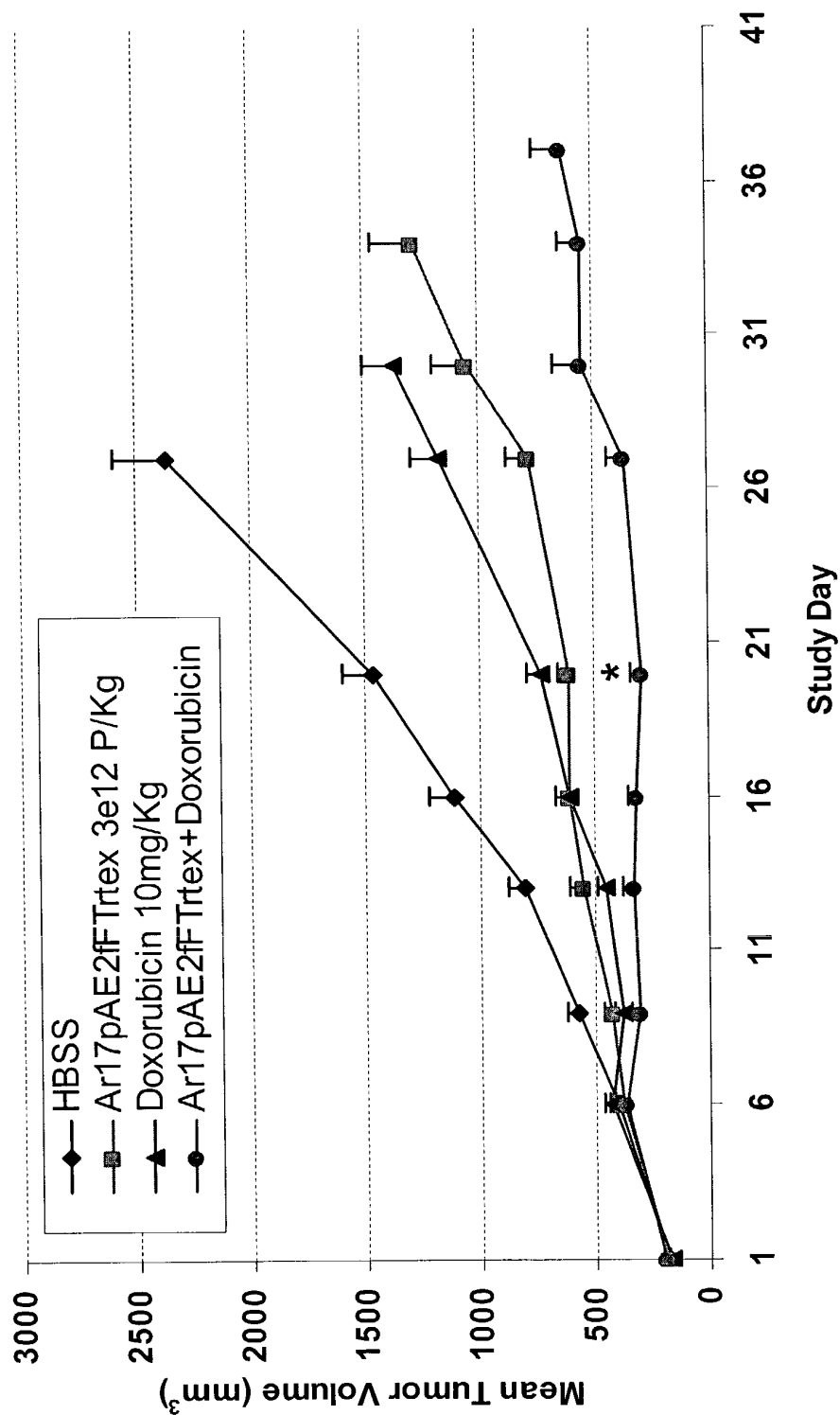
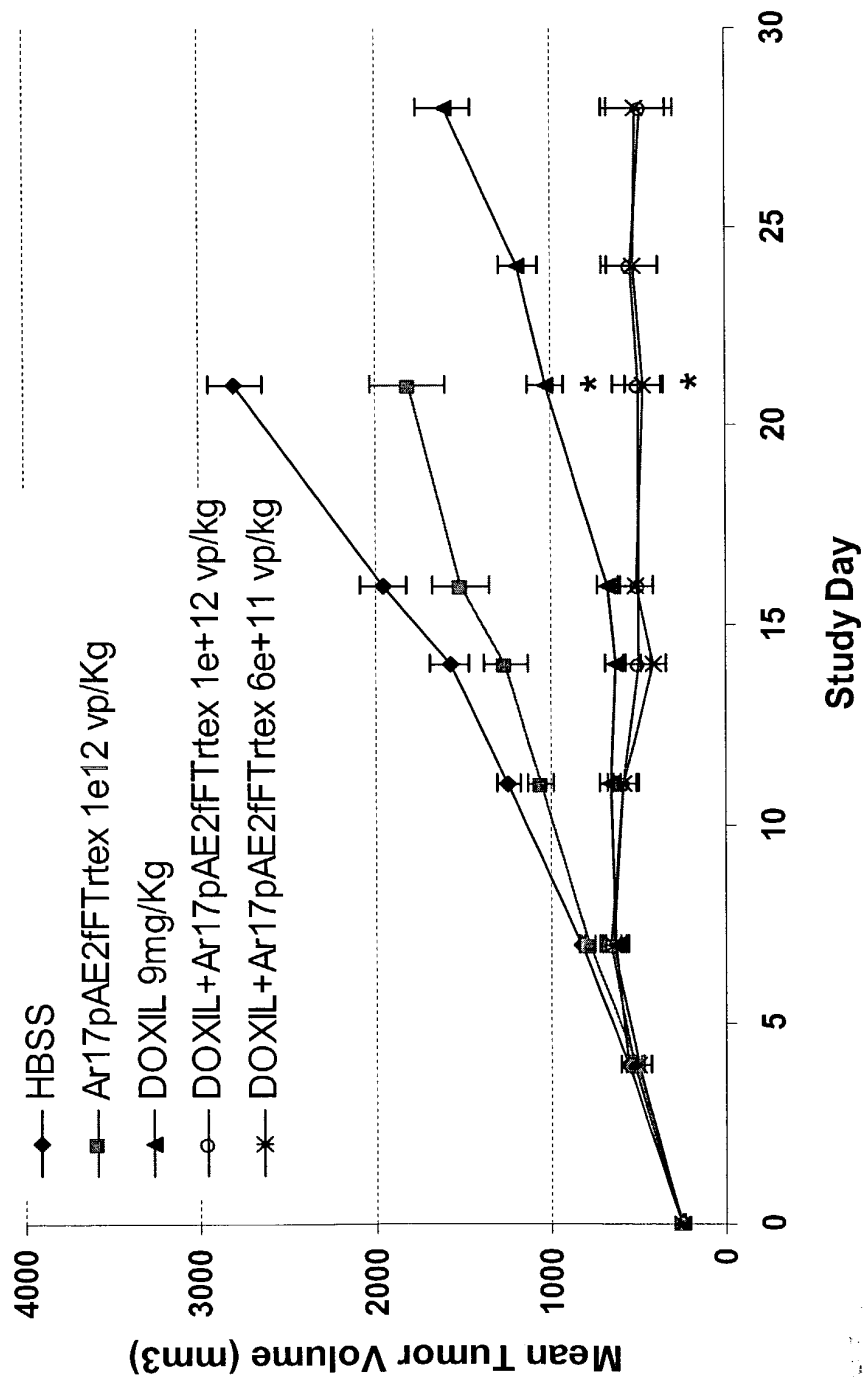
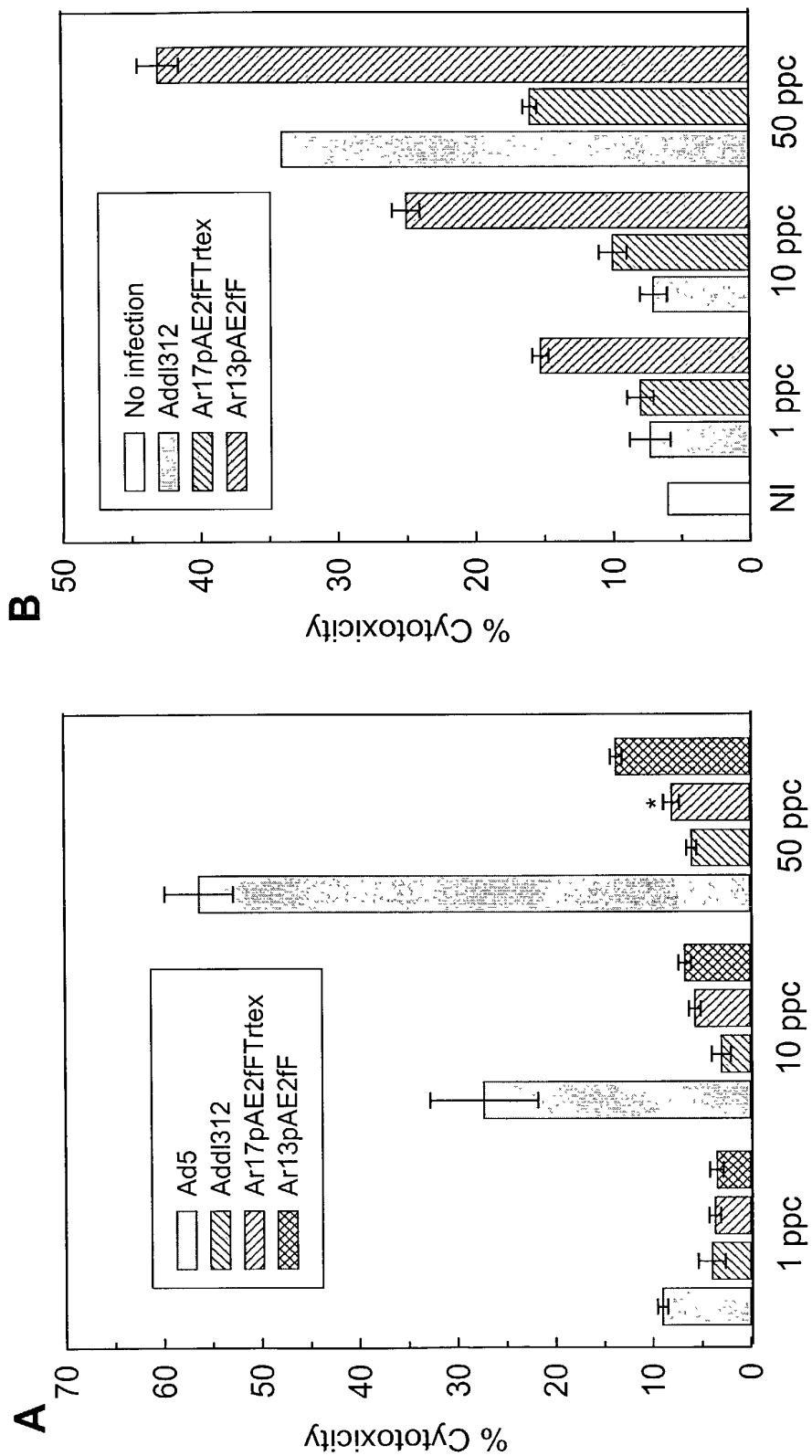


Figure 67



1. The method of claim 1, wherein the tumor is a solid tumor.

Figure 68



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Figure 69

Ad35-Based Oncolytic Vectors

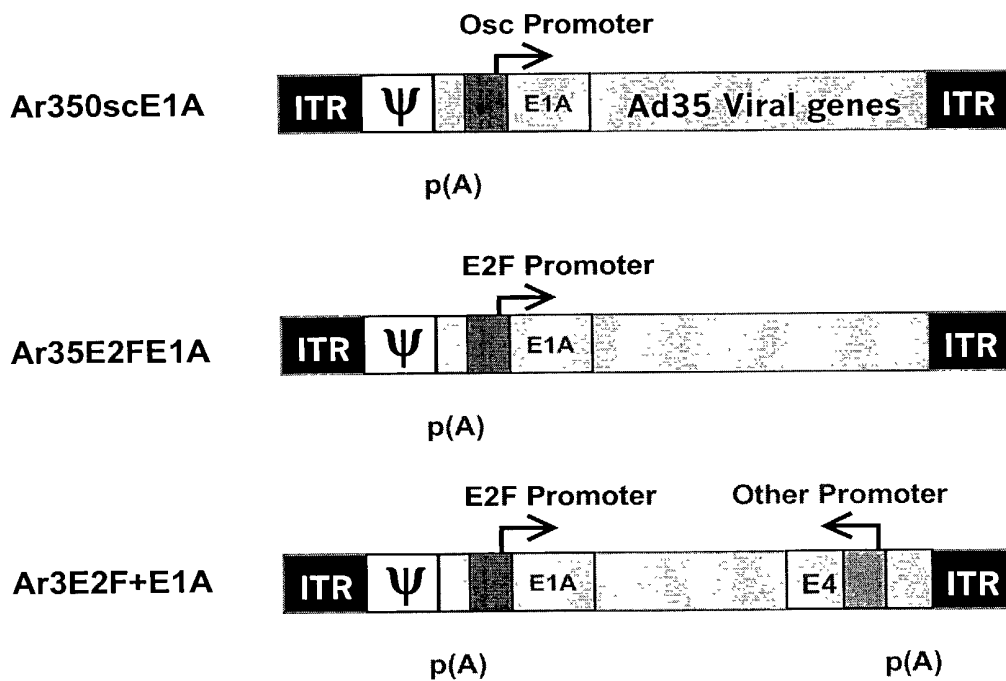


Figure 70

